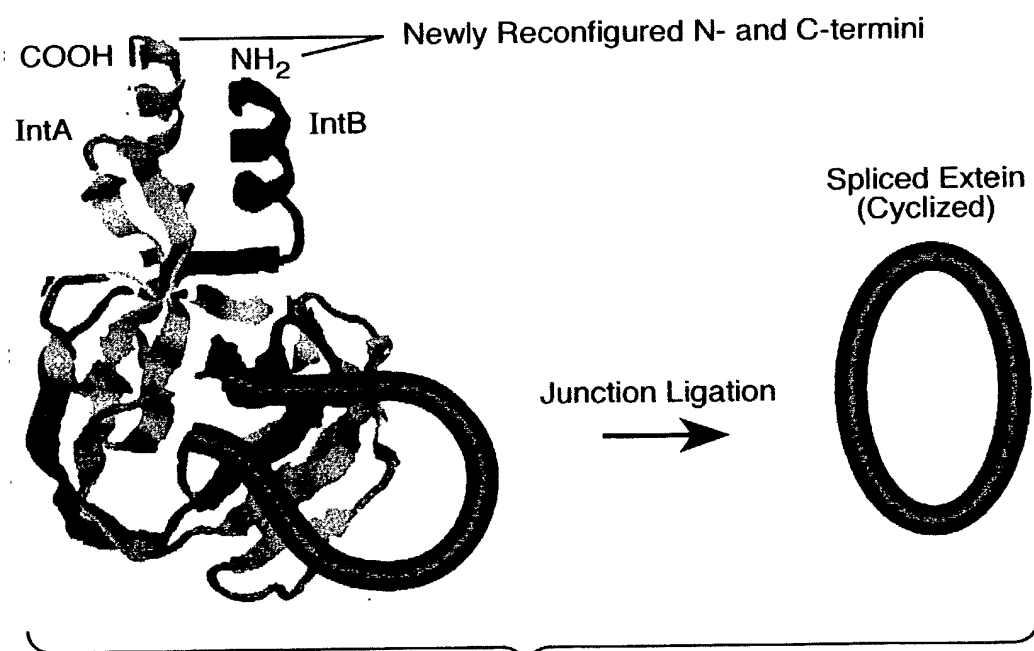
**FIG. 2A****FIG. 2B**

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GCISGDSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLES AKVSRVFCTGKKLVYILKT  
 RLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLMSDEELGLLGHLIGDGC  
 TLPRHAIQYTSNKIELAEKVVELAKAVFGDQINPRISQERQWYQVYIPASYRLTHNKNPIT  
 KWLENLDVFGFLRSYEFVFNQVFEQPQRAIAIFLRHLWSTDGCVKLIVEKSSRPVAYYATSS  
 EKLAKDVQSLLLKLGINARLSKISQNGKGRDNYHVTITGQADLQIFVDQIGAVDKDKQASVE  
 EIKTHIAHQANTNRDVIPKQIWKTYVLPQIQIKGITTRDLQMLGNAYCGTALYKHNSLSRE  
 RAAKIATITQSPEIEKLSQSDIYWDSIVSITETGVEEVFDLTVPGPHNFVANDIIVHNS

**FIG.\_3A**

YCITGDALVALPEGESVRIADIVPGARPNSDNAIDLKVLDRHGNPVLADRLFHSGEHPVYTV  
 RTVEGLRVGTANHPLLCLVDVAGVPTLLWKLIDEIKPGDYAVIQRSASFVDCAGFARGKPE  
 FAPTTYTVGVPGLVRFLFAHHRDPDAQAIADELTDGRFYAKVASVTDAGVQPVYSLRVDTA  
 DHAFITNGFVSHNT

**FIG.\_3B**

ECLTSDHTVLTTRGWIPIADVTLDDKVAVLDNNTGEMSYQNPQKVHKYDYEGLPMYEVKTAGV  
 DLFVTPNHRMYVNTTNNTNQNYNLVEASSIFGKKVRYKND AIWNKTDYQFILPETATLTGH  
 TNKISSTPAIQPEMNAWLTFGLWIANGH TT KIAEKTAENNQQKQRYKVILTQVKEDVCDII  
 EQTLNKLGFNFIRSGKDYTIENKQLWSYLNPF DN GALNKYLPDWVWELSSQQCKILLNSLCL  
 GNCLFTKNDDTLHYFSTSERFANDVSRLALHAGTTSTIQLEAAPS NLYDTIIGLPVEVNTTL  
 WRVIINQSSFYSYSTDKSSALNLSNNVACYVNAQSALTLEQNSQKINKNTLVLTKNVKSQT  
 MHSQRAERVD TALLTQKELDNSLNHEILINKNPGTSQLECVVNPEVNN TSTNDRFVYYKGPV  
 YCLTGPNNVFYVQRNGKAVWTGNS

**FIG.\_3C**

LCVAPETMILTEDGQFP IKDLEGGKIIKVWNGNEFSSVTVVKTGTEKELLEVE LSNGCTL SCT  
 PEHKFIIVKSYTEAKKQKTDDNAIANAERVDAQDLKPRMKLIKFDLPTLFGNSEHDIKYPYT  
 HGFFCGDGTYTKYKGPQLSLYGDKKELLTYLDVRTMTGLE DASGR LNTWLPLDLAPKFDVPI  
 NSSLECRM EWLAGYLDADGCVFRNGT NESIQVSCIHLDFLKRIQLLLIGMGVTSKITKLHDE  
 KITTMPDGKGGQKPYSCKPIWRLFISSSGLYHLSEQGFETRRLKWEPRQPQRNAERFVEVLK  
 VNKTGRVDDTYCFTEPINHAGVFNGILTQC

**FIG.\_3D**

GCFTKGTQVMMADGADKSIESIEVGDKVMGKDGM PREVVGLPRGYDDMYKVRQLSSTRNAK  
 SEG LMDFTVSADHKLILKTKQDVKIATR KIGGNTYTGVTFYVLEKTKTGIELVAKTKVFGH  
 HIHGQNGAEKAATFAAGIDSKEYIDWII EARDYVQVDEIVKTSTTQMINPVHFESGKLG NW  
 LHEHKQNKSLAPQLGYLLGTWAGIGNVKSSAFTMNSKDDVKLATRIMNYSSKLGMTCSSTES  
 GELNVAENEEFFNNLGAEKDEAGDFTFDEFTDAMDELTINVHGAAASKKNLLWNALKSLG  
 FRAKSTDIVKSIPQHIAVDDIVVRESLIAGLVDAAGNVETKSN GSIEAVVRTSFRHVARGLV  
 KIAHSLGI ESSINIKDTHIDAAGVRQEFACIVNL TGAPLAGVLSKALARNQTPVVKFTRDP  
 VLFNFDLIKSAKENYYGITLAEETHQFLLSNMALVHNC

**FIG.\_3E**

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GCLSYATNQPYFLKSDNVNFSKLTSLKVSNNHYILSATLELLIPFQYNRIYPIVSLIKRELQT  
 GYKVYELDFYISVIVSTVEHYVLTNGWKRILELTVDDLVA TLDIQYLIYNNTEVDLFSSN  
 VIFSSVINLICMNRINVYDFWIPKTNNFFVNALLVHNS

**FIG.\_3F**

GCISKFSHIMWSHVSKPLFNFSIKKSHMHNFNKNYQLLDQGEAFISRQDKKTTYKIRTNSE  
 KYLELTSNHKILTLRGWQRCDQLLCNDMITTQIGFELSRKKKYLNCIPFSLCNFETLANIN  
 ISNFQNVDFFAANPIPNFIANNIIVHNS

**FIG.\_3G**

GCFAGTNVLMADGSIECIENIEVGNKVMGKDGRPREVIKLPRGRETMYSVVQKSQHRAHKS  
 DSSREVPELLKFTCNATHELVVRTPRSVRRLSRTIKGVEYFEVITFEMGQKKAPDGRIVELV  
 KEVSKSYPISEGERANELVESYRKASNKAYFEWTIEARDLSLLGSHVRKATYQTYAPILYE  
 NDHFFDYMQKSKFHLTIEGPKVLAYLLGLWIGDGLSDRATFSVDSRDTSLMERVTEYAEKLN  
 LCAEYKDRKEPQVAKTVNLYSKVVRGNGIRNNLNNTENPLWDAIVGLGFLKDGVKNI PSFLST  
 DNIGTRETFLAGLIDSDGYVTDEHGKATIKTIHTSVRDGLVSLARSLGLVSVNAEPAKVD  
 MNGTKHKISYAIYMSGGDVLLNVLSKCAGSKKFRPAPAAFARECRGFYFELQELKEDDYG  
 ITLSDDSDHQFLLANQVVVHNC

**FIG.\_3H**

GCFAYGTRGALADGTTEKIGKIVNQKMDVEVMSYDPD TDQVVPRKVVNWFNNGPAEQFLQFT  
 VEKSGGNGKSQFAATPNHLIRTPAGWTEAGDLVAGDRVMAAEPHRLSDQQFQVVLGSLMGDG  
 NLSPNRRDRNGVRFRMGHGAKQVDYLQWKTALLGNIKHSTHVNDKGATFVDFTPLPELAELQ  
 RAVYLGDGKKFLSEENFKALTPLALVFWMDDGPFTVRSKGLQERTAGGSGRIEICVEAMSE  
 GNRIRLRDYL RDTHGLDVRLRLSGAAGKSVLVFSTASSAKFQELVAPYITPSMEYKLLPRFR  
 GQGAVTPQFVEPTQRLV PARVLDVHVKPHTRSMNRFDIEVEGNHNYFVDGVMVHNS

**FIG.\_3I**

YCLSFGTEILTVEYGPLPIGKIVSEEINCSVYSVDPEGRVYTQAI AQWHD RGEQEVLEYELE  
 DGSVIRATSDHRFLT TDYQLLAIEEIFARQLDLLTLENIKQTEEALDNHRLPFPLLDAGTIK

**FIG.\_3J**

KALALDTPLPTPTGWTAMGDVAVGDELLAVDEAPTRVVAATEV MLGRPCYEIEFS DGTVIVA  
 DAQH QWPTS YGIRTS AQLRCGLDIIAAAGSTPRHAGRLTTAAFMAPVLCIDSVRRVRSVPVR  
 CVEVDNA AHLYL AGRGMVPTHNS

**FIG.\_3K**

GALAYDEPIYLS DGNII NIGEFVDKFFK KYKNS IKKEDNGFGWIDIGNENIYIKSFNKLSLI  
 IEDKRILRVWRKKYS GKLIKITTKNRREITLTHDHPVYISK TGEVLEINAEMVKVGDIYIP  
 KNNTINLDEVIKVETVDYNGHIYDLTVEDNHTYIAGKNEGFAVSNC

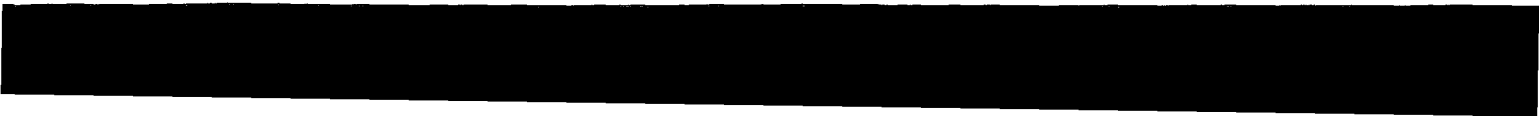
**FIG.\_3L**

**FIG. 3M**

**FIG. 3N**

**FIG. 30**

**FIG. 3P**



**FIG.\_3Q**

**FIG. 3R**

**FIG. 3S**

**FIG.\_3T**

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KCLTGDTKVIANGQLFELRELVEKISGGKFGPTPVKGLKVGIGIDEDGKLREFEVQYVYKDKT  
 ERLIRIRTRLGRELKVTPYHPLLNNRRNGEIKWVKAEEELKPGDKLAVPRFLPIVTGEDPLAE  
 WLGYFLGGGYADSKENLIMFTNEDPLLQRQFMELTEKLFSDARIREITHENGTSKVYVNSKK  
 ALKLVNSLGNNAHIPKECWGRGIRSFRLAYFDCNGGVKGNAIVLATASKEMSQEIAYALAGFGI  
 ISRIQEYRVIIISGSDNVKKFLNEIGFINRNKLEKALKLVKKDDPGHDGLEINYELISYVKDR  
 LRLSFFNDKRSWSYREAKEISWELMKEIYYRLDELEKLKESLSRGILIDWNEVAKRIEEVAE  
 ETGIRADELLEYIEGKRKLSFKDYIKIAKVLGIDVEHTIEAMRVFARKYSSYAEIGRRLGTW  
 NSSVKTILESNAVNEILERIRKIELELIEEILSDEKLKEGIAYLIFLSQNELYWDEITKVE  
 ELRGEFIIYDLHVPGYHNFIAGNMPTVVHNT

**FIG.\_3U**

SCVTGDTKVYTPDEREVKIRDFMNYFENGLIKEVSNRIGRDTVIAAVSFNSRIVGHPVYRLT  
 LESGRIIEATGDHMF LTPEGWKQTYDIKEGSEVLVKPTLEGTPYEPDPRVIIDIKEFYNFLE  
 KIEREHNKPLKEAKTFRELITKDKEKILRRALELRRAEIEENGLTKREAEILELISADTWIPR  
 AELEKKARISRTRLNQILQRLEKKGYIERRIEGRKQFVRKIRNGKILRNAMDIKRILEEEFG  
 IKISYTTVKLLSGNVDMAYRILKEVKEKWLVRDYDEKAGILARVVGFI LGDGH LARNGRI  
 WFNSSKEELEMLANDLRKLGLKPSEI IERDSSSEIQGRKVKGRIMLYVDNAAFHALLRFWK  
 VEVGNKTKKGYTVPEWIKKGNLFVKREFLRGLFGADGTPKPCGKRYNFGIKLEIRAKKESLE  
 RTVEFLNDVADLLREFDVDSKITVSP TKEGFIIRLIVTPNDANYLNFLTRVGYAYAKDTYAR  
 LVGEYIRIKLAYKNIILPGIAEKAIELATVTNSTYAAKVLGVSRDFVVRNLKGTQIGITRDF  
 MTFEEFMKERVNLNGYVIEKVIKKEKLG YLDVYDVT CARDHSFISNGLVSHNC

**FIG.\_3V**

NCLTSNSKILTDDGYYIKLEKLKEKLDLHIKIYNTEEGEKSSNILFVSERYADEKIIIRIKTE  
 SGRVLEGSKDHPVLT LN GYVPMGMLKEGDDVIVYPYEGVEYEEPSDEIILDEDDFAEYDKQI  
 IKYLDKDRGLPLRMDNKNIGIIARLLGFAFGDGSIVKENGDRERLYVAFYGKRETLIKIRE  
 LEKLGIKASRIYSRKREVEIRNAYGDEYTS LCEDNSIKITSKAFALFMHKLGMPIGKKTEQI  
 YKIPEWIKKAPKWVRNFLAGLFGADGSRAVFKNYTPLPINLTMSKSEELKENILEFLNEIK  
 LLLAEFDIESMIYEIKSLDGRVSYRLAIVGEESIKNFLGRINYEYSGEKKVIGLLAYEYLR  
 KDIKEIRKKCIKRAKELYKKGVTVSEMLKMDEF RNEFISKRLIERAVYENLDEDDVRISTK  
 FPKFEEFIEKYGVIGGFVIDKIKEIEEISYDSKLYDVGVISKEHNF IANSIVVHNC

**FIG.\_3W**

KCVDGDTLVLTKEFGLIKIKELYEKLDGKGRKIVEGNEEWTELEKPITVYGYKDGKIVEIKA  
 THVYKGVSSGMVEIRTRTGRKIKVTP IHR LFTGRVTKDGLILKEVMAMHVKPGDRIAVVKKI  
 DGGEYIKLDSSNVGEIKVPEILNEELAEFLGYLMANGTLKSGIIEIYCDDDESLLERVNSLSL  
 KLFGVGGRIVQKVDGKALVIQSKPLVDVLRRLGVPEDKKVENWKVPRELLS P SNVVRAFN  
 AYIKGKEEVEITLASEEGAYELSYLFAKLG IYVTISKSGEYYKVRVSRRGNLDTIPVEVNGM  
 PKVLPYEDFRKFAKSIGLEEVAENHLQHII FDEVIDVRYIPEPQEVYDVT TETHNFVGGNMP  
 TLLHNT

**FIG.\_3X**



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*Intein B*

MESG[SPEIEKLSQSDIYWDSIVSITETGVEEVFDLTVPGPHNFVAND

*Cyclid Insert (With Flagg Epitope)*

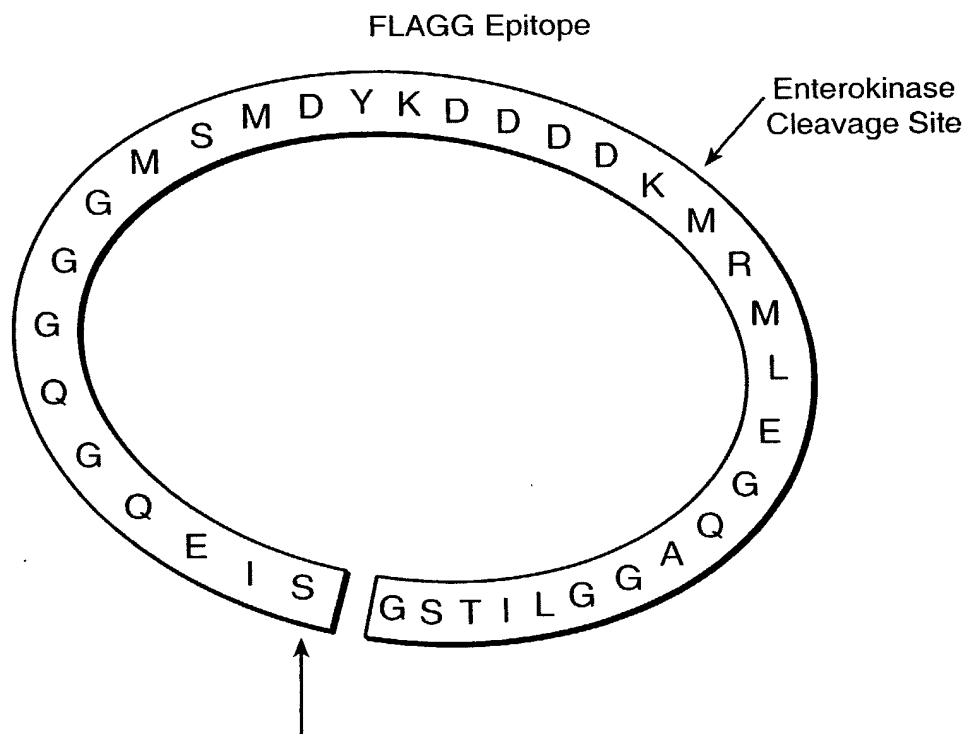
IIVHN[SIEQGQGGGMSMDYKDDDDKMRMLEGQAGGLITS[G]CIS

GDSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLESKVS RVFCT

*Intein A*

GKKLVYILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRK

LESSSLQLS IHGYH



This is the only Invariant Extein-encoded Amino Acid  
(Depending on Intein used this can be a Cysteine, Serine or Theronine).

**FIG. 4A**

CMV Promoter →

1 / 1 31 / 11  
 GCT TCG CGA TGT ACG GGC CAG ATA TAC GCG TTG ACA TTG ATT ATT GAC TAG TTA TTA ATA  
 121 / 41 151 / 51  
 TAC GGT AAA TGG CCC GCC TGG CTG ACC GCC CAA CGA CCC CCG CCC ATT GAC GTC AAT AAT  
 241 / 81 271 / 91  
 TTT ACG GTA AAC TGC CCA CTT GGC AGT ACA TCA AGT GTA TCA TAT GCC AAG TAC GCC CCC  
 361 / 121 391 / 131  
 GGA CTT TCC TAC TTG GCA GTA CAT CTA CGT ATT AGT CAT CGC TAT TAC CAT GGT GAT GCG  
 401 / 161 511 / 171  
 CCA CCC CAT TGA CGT CAA TGG GAG TTT GTT TTG GCA CCA AAA TCA ACG GGA CTT TCC AAA  
 601 / 201 631 / 211  
 CTA TAT AAG CAG AGC TCT CTG GCT AAC TAG AGA ACC CAC TGC TTA CTG GCT TAT CGA AAT  
 721 / 241 751 / 251  
 CTG tcg act GGA GGA ACC ATG GAG TCC GGA M E S G tca cca gaa ata gaa aag ttg tct cag agt  
 841 / 281 871 / 291  
 ttg act gtg cca gga cca cat aac ttt gtc ggc aat gac atc att gtc cat aac L T V P G P H N F V A N D I V H N agt ATC  
 961 / 321 991 / 331  
ATG ctc gag ggc caa gca ggt gga CTG ATC ACC agt ggc TGC ATC AGT GGA GAT AGT ttg  
 1081 / 361 1111 / 371  
 ttt gaa ata tgg gca att aat gaa cag acg atg aag cta gaa tca gct aaa gtt agt cgt  
 1201 / 401 1231 / 411  
 aag gca aca gca aat cat aga ttt tta act att gat ggt tgg aaa aga tta gat gag cta  
 1321 / 441 1351 / 451  
GAT cca tgg tta cca TGA caa ttg GCG GCC GCT CGA GTC TAG AGG GCC CGC GGT TCG AAG  
 1441 / 481  
 ATC ACC ATT GAG TTT AAA CCC GCT GAT

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FIG..4B-1

61 / 21	91 / 31
GTA ATC AAT TAC GGG GTC ATT AGT TCA TAG CCC ATA TAT GGA GTT CCG CGT TAC ATA ACT	
181 / 61	211 / 71
GAC GTA TGT TCC CAT AGT AAC GCC AAT AGG GAC TTT CCA TTG ACG TCA ATG GGT GGA CTA	
301 / 101	331 / 111
TAT TGA CGT CAA TGA CGG TAA ATG GCC GCG CTG GCA TTA TGC CCA GTA CAT GAC CTT ATC	
421 / 141	451 / 151
GTT TTG GCA GTA CAT CAA TGG GCG TGG ATA GCG GTT TGA CTC ACG GGG ATT TCC AAG TCT	
541 / 181	571 / 191
ATG TCG TAA CAA CTC GCG CCC ATT GAC GCA AAT GGG CGG TAG GCG TGT ACG GTG GGA GGT	
661 / 221	691 / 231
TAA TAC GAC TCA CTA TAG GGA GAC CCA AGC TGG CTA GTT AAG CTT cct ata cta gga GAT	
781 / 261	811 / 271
gat att tac tgg gac tcc atc gtt tct att acg gag act gga gtc gaa gag gtt ttt gat	IntB (IC)
D I V W D S I V S I T E T G V E E V F D	
901 / 301	931 / 311
Flag Epitope Insert	
GAA CAA ggc cag ggc ggt ggc ATG TCA ATG gac tat aaa gat gac gat aag ATG AGG	
E Q G Q G G G M S M D Y K D D D K M R	
1021 / 341	1051 / 351
atc agc ttg gcg agc aca gga aaa aga gtt tct att att aaa gat ttg tta gat gaa aaa gat	
I S L A S S T G K K R R V S I K D L L D E K D	
1141 / 381	1171 / 391
IntA (IN)	
gta ttt tgt act ggc aaa aag cta gtt tat gtt tta aaa act cga cta ggt aga act atc	
V F C T G K K K L V Y I L K K T R L L G R T I	
1261 / 421	1291 / 431
tct tta aaa gag cat att gct cta ccc cgt aaa cta gaa agc tcc tct tta caa tta ATC	
S L K E H I A L P R K L L E S S S L Q L I	
1381 / 461	1411 / 471
GTA AGC CTA TCC CTA ACC CTC TCC TCG GTC TCG ATT CTA CGC GTA CCG GTC ATC ATC ACC	

FIG..4B-2

FIG..4B

FIG..4B-1

FIG..4B-2

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ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTTGACTGTGCCAGGGCCCCATA  
ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG  
CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAA  
CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
TCGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC  
CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCCTGAAGTTCATCTGCACCACC  
GGCAAGCTGCCCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT  
CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT  
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
CGGCAACATCCTGGGGCACAAGCTGGAGTACAACACTACAACAGCCACAACGTCTATATCATGG  
CCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACCTC  
GAGCAAAAGCTGATATGCATCTCCGGAaATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG  
AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA  
CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAGCTAGTTTAT  
ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT  
TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAGAGCATATTGCTCTACCCCGTAAAC  
TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC  
GCTATCGATTAA

**FIG.\_5A**

MESGSPEIEKLSQSDIYWDSIVSITETGVVEEVFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ  
LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG  
SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT  
GKLPVPWPPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV  
KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDL  
EQKLICISGNSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLES AKVSRVFC TGKKLVY  
ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
AIDZ

**FIG.\_5B**

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ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTGACTGTGCCAGGGCCCCATA  
ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG  
CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAA  
CCACTACCTGAGCACCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
TCGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC  
CGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACC  
GGCAAGCTGCCCCGTGCCCTGGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT  
CAGCCGCTACCCCGACCACATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCCGAAGGCT  
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
TGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCATC  
GTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTGACTGTGCCAGGGCCCCATAA  
CTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAGC  
TCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAA  
CACTACCTGAGCACCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGT  
CCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGGT  
CGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTACC  
GGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTC  
CGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCG  
GCAAGCTGCCCCGTGCCCTGGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT  
AGCCGCTACCCCGACCACATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCCGAAGGCTA  
CGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGA  
AGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGAC  
GGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACAGCCACAACGTCTATATCATGGC  
CGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACCTCG  
AGCAAAAGCTGATATGCATCTCCGGAATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAGA  
GTTTCTATTAAAGATTGTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGAC  
GATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTGTACTGGCAAAAGCTAGTTTATA  
TTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAAATTTTAACTATT  
GATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAGAGCATATTGCTCTACCCCGTAACT  
AGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTACG  
CTATCGATTAA

FIG.\_5C

MESGSPEIEKLSQSDIYWDSIVSITETGVEEVFDLTPGPHNFVANDIIVHNSEEDLGSSVQ  
LADHYQONTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG  
SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGECDATYGLTLTKFICTT  
GKLPVPWPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV  
KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDL  
EQKLICISGNSLISLASTGKRVSIDLLDEKDFEIWAINETMKLESASVSRVFTGKKLVY  
ILKTRLGRTIKATANHKFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
AIDZ

FIG.\_5D

**FIG. 5E**

**FIG. 5F**

**FIG. 5G**

**FIG. 5H**

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ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
CGTTcCTATTACGGGAGACTGGAGTCGAAGAGGTTTTTGATTTGACTGTGCCAGGGCCCCATA  
ACTTTGTGGCCAATGACATCATTTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG  
CTCGCCGACCCTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAA  
CCACTACCTGAGCACCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
TCGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC  
CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCCTGAAGTTCATCTGCACCACC  
GGCAAGCTGCCCCGTGCCCTGGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT  
CAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCCGAAGGCT  
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
CGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCATATCATGG  
CCGACAAGCAGAAGAACGGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGGACCTC  
GAGCAAAAGCTGATATGCATCTCCGGAaATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG  
AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA  
CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT  
ATTTTAAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT  
TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAGAGCATATTGCTCTACCCCGTAAAC  
TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC  
GCTATCGATTAA

**FIG.\_5I**

MESGSPEIEKLSQSDIYWDSIVPITETGVVEEFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ  
LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG  
SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT  
GKLPVPWPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV  
KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDL  
EQKLICISGNSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLESAKVS RVFCTGKKLVY  
ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
AIDZ

**FIG.\_5J**



ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTTGACTGTGCCAGGGCCCCATA  
ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG  
CTCGCCGACCCTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAA  
CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
TCGAACGGGGAAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTCAC  
CGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC  
GGCAAGCTGCCCCGTGCCCTGGCCACCCCTCGTGACCACCCCTGACCTACGGCGTGCAGTGCTT  
CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT  
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
CGGCAACATCCTGGGGCACAAGCTGGAGTACAAC TACAACAGCCACAACGTCTATATCATGG  
CCGACAAGCAGAAGAACGGCATCAAGGTGAAC TCAAGATCCGCCACAACATCGAGGACCTC  
GAGCAAAAGCTGATATGCATCTCCGGAaATAGTTTGATCAGCTTGCGCAGCACAGGAAAAAG  
AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA  
CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAgGCTAGTTTAT  
ATTTTAAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTTTAACTAT  
TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAAGAGCATATTGCTCTACCCCGTAAAC  
TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC  
GCTATCGATTAA

**FIG.\_5K**

MESGSPEIEKLSQSDIYWDSIVSITETGVEEVFDLTPVGP HNFVANDIIVHNSEEDLGSSVQ  
LADHYQQNTPIGDPVLLPDNHYLSTQSALS KDPNEKRDHMV LLEFVTAAGITLGMDELYKG  
SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLT LKFICTT  
GKLPVPWPTLVTTLTYGVQCF SRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRA EV  
KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNF KIRHNIEDL  
EQKLICISGNSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLES AKVSRVFCTGKRLVY  
ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
AIDZ

**FIG. 5L**

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ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTTGACTGTGCCAGGGCCCCATA  
ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG  
CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAA  
CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
TCGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC  
CGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC  
GGCAAGCTGCCCCGTGCCCTGGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT  
CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCCGAAGGCT  
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
CGGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACAGCCACAACGTCCTATATCATGG  
CCGACAAGCAGAAGAACGGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGGACCTC  
GAGCAAAAGCTGATATGCATCTCCGGAGATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG  
AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA  
CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT  
ATTTTAAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAAATTTTAACTAT  
TGATGGTTGAAAAAGATTAGATGAGCTATCTTTTAAAGAGCATATTGCTCTACCCCGTAAAC  
TAGAAAGCTCCTCTTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC  
GCTATCGATTAA

**FIG.\_5M**

MESGSPEIEKLSQSDIYWDSIVSITETGVVEEVDLTVPGPHNFVANDIIVHNSEEDLGSSVQ  
LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG  
SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT  
GKLFPVPWPTLVTTLTLYGVQCFSTRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV  
KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDL  
EQKLICISGDSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLESAKVS RVFCTGKKLVY  
ILKTRLGRTIKATANHKFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
AIDZ

**FIG.\_5N**

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ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
CGTTcCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTTGACTGTGCCAGGGCCCCATA  
ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG  
CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAA  
CCTACTCTGAGCACCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
TCGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC  
CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCCTGAAGTTCATCTGCACCACC  
GGCAAGCTGCCCCGTGCCCTGGCCACCCCTCGTGACCACCCCTGACCTACGGCGTGACGTGCTT  
CAGCCGCTACCCCGACCACATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCCGAAGGCT  
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
AAGTTCGAGGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
CGGCAACATCCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACGTCTATATCATGG  
CCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACCTC  
GAGCAAAAAGCTGATATGCATCTCCGGAGATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG  
AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA  
CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT  
ATTTTAAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT  
TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAGAGCATATTGCTCTACCCCGTAAAC  
TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC  
GCTATCGATTAA

**FIG.\_50**

MESGSPEIEKLSQSDIYWDSIVPITETGVVEVFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ  
LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG  
SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT  
GKLPVPWPPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV  
KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDL  
EQKLCISGDSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLES AKVSRVFCTGKKLVY  
ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
AIDZ

**FIG.\_5P**

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ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT  
CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTTGACTGTGCCAGGGCCCCATA  
ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG  
CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAA  
CCTACTACCTGAGCACCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG  
TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG  
TCGAACGGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC  
CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT  
CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC  
GGCAAGCTGCCCCGTGCCCTGGCCACCCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT  
CAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCCGAAGGCT  
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG  
AAGTTCGAGGGCGACACCCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA  
CGGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACAGCCACAACGTCATATCATGG  
CCGACAAGCAGAAGAACGGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGGACCTC  
GAGCAAAAGCTGATATGCATCTCCGGAGATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG  
AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAGTTAATGAACAGA  
CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTAAGTGGCAAAAGCTAGTTTAT  
ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT  
TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAGAGCATATTGCTCTACCCCGTAAAC  
TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC  
GCTATCGATTAA

**FIG.\_5Q**

MESGSPEIEKLSQSDIYWDSIVSITETGVVEVFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ  
LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG  
SNGEFSQVDKSMVSKGEELFTGVVPIILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT  
GKLPVPWPPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV  
KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDL  
EQKLICISGDSLISLASTGKRVS IKDLLDEKDFEIWAVNEQTMKLESAKVS RVFCTGKKLVY  
ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY  
AIDZ

**FIG.\_5R**



**FIG. 6B**

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GAT ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CTG GTC GAG CTG
D M V S K G G E E L F T G V V L L V E L
TAC GGC AAG CTG ACC CTG AAG TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC
Y G K L T L L K F I C T T G K K V V P W P
AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG CGC ACC ATC
K Q H D F F F A M P E G Y V Q R T I
CTG GTG AAC GCG ATC GAG CTG AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG
L V N R I I E L K K G G I D G F K K E D G G N I L G
AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC GTG CAG CTC
N G I K V N F K I I R H N I I E D G S V Q L
CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATC
H Y L S S Q S A L S K D P N E K R D H M

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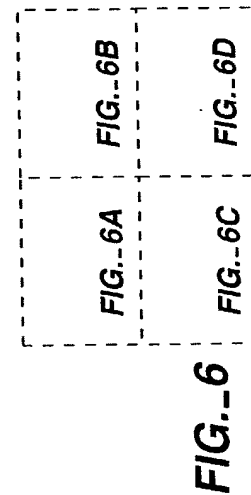
TAA
*

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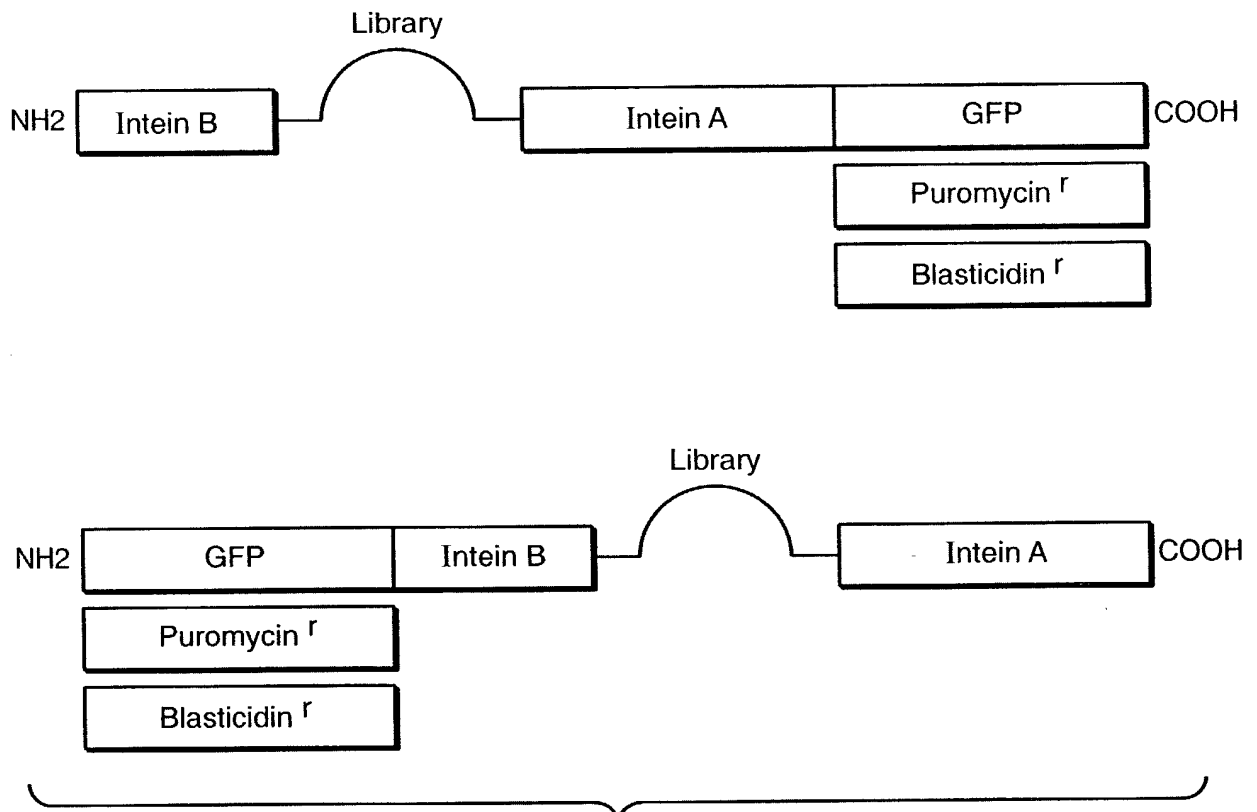
FIG.\_6C

GAC D	GGC G	GAC D	GAC V	GTA V	AAC N	AAC G	GGC G	CAC H	AAC K	TTC F	AGC S	GTG V	TCC S	GGC G	GAG E	GGC G	GAT D	GCC A	ACC T
ACC T	CTC L	GTG V	ACC T	GTG V	ACC T	CTG L	ACC T	TAC Y	GGC G	TTC F	AGC S	GTG V	CAG Q	TTC F	AGC S	CGC R	TAC Y	CCC P	ATG M
TTC F	TTC F	AAG K	GAC D	GAC D	GAC D	GAC G	GGC N	AAC Y	TAC K	AAG T	ACC R	CGC A	GGC E	GTG K	AAG F	TTC E	TTC G	GAG D	GGC T
CAC H	AAG K	CTG L	GAG E	GAG E	TAC Y	AAC N	TAC Y	AAC N	AGC S	CAC H	AAC N	ATC I	TAT Y	ATG M	GCC A	GAC D	AAG K	CAG Q	AAG K
GCC A	GAC D	CAC H	CAC H	TAC Y	CAG Q	CAG Q	ACC N	ACC T	CCC P	ATC I	GGC G	GAC D	GGC G	CTG V	CCC P	CTG L	CCC P	GAC D	AAC N
GTC V	CTG L	CTG L	GAG E	GAG E	TTC F	GTG V	ACC T	ACC A	GGC A	GGG G	ATC I	ACT T	CTC L	GGC G	ATG M	GAG E	CTG L	TAC Y	AAG K

**FIG. 6D**

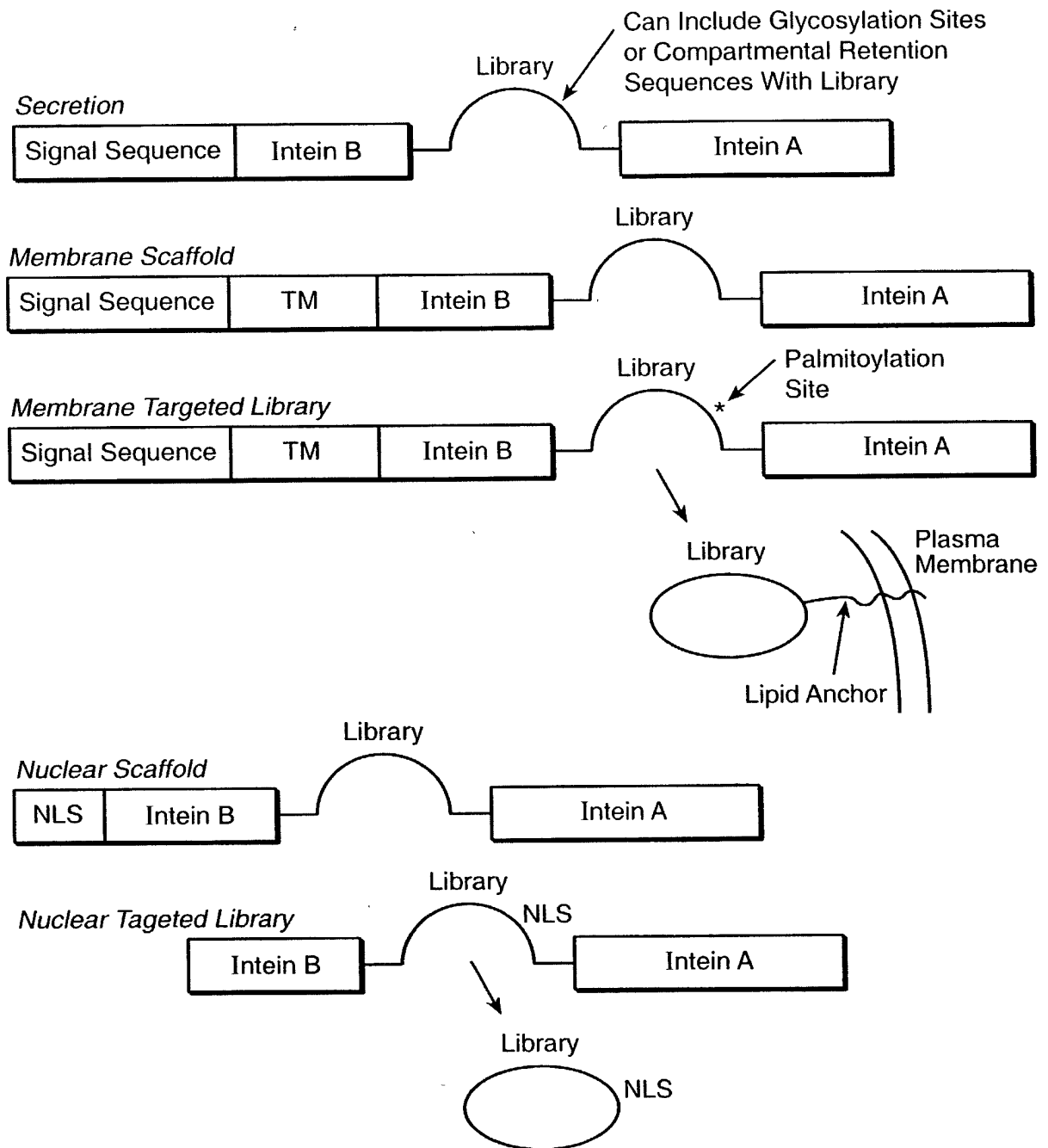




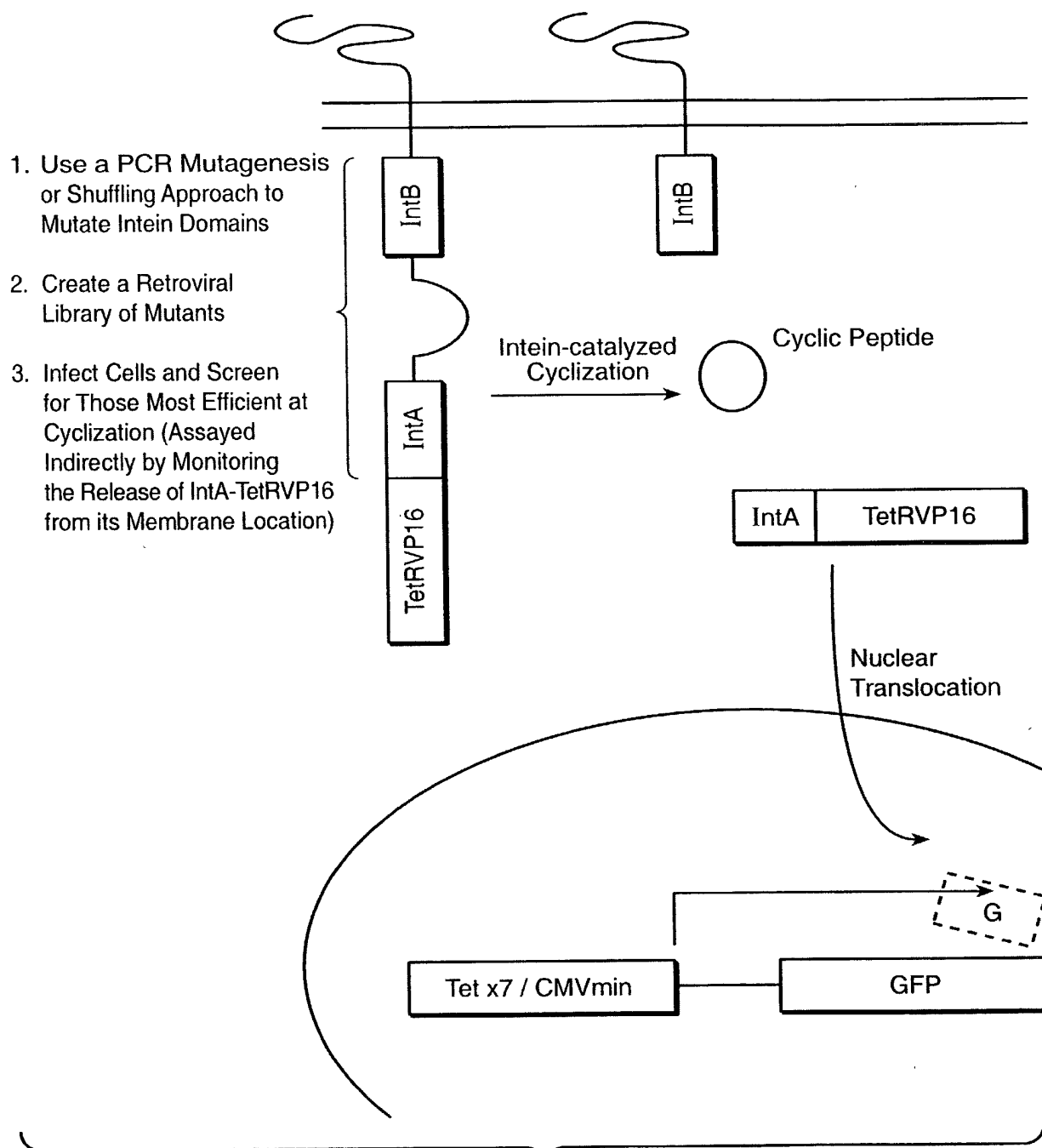


**FIG. 7**

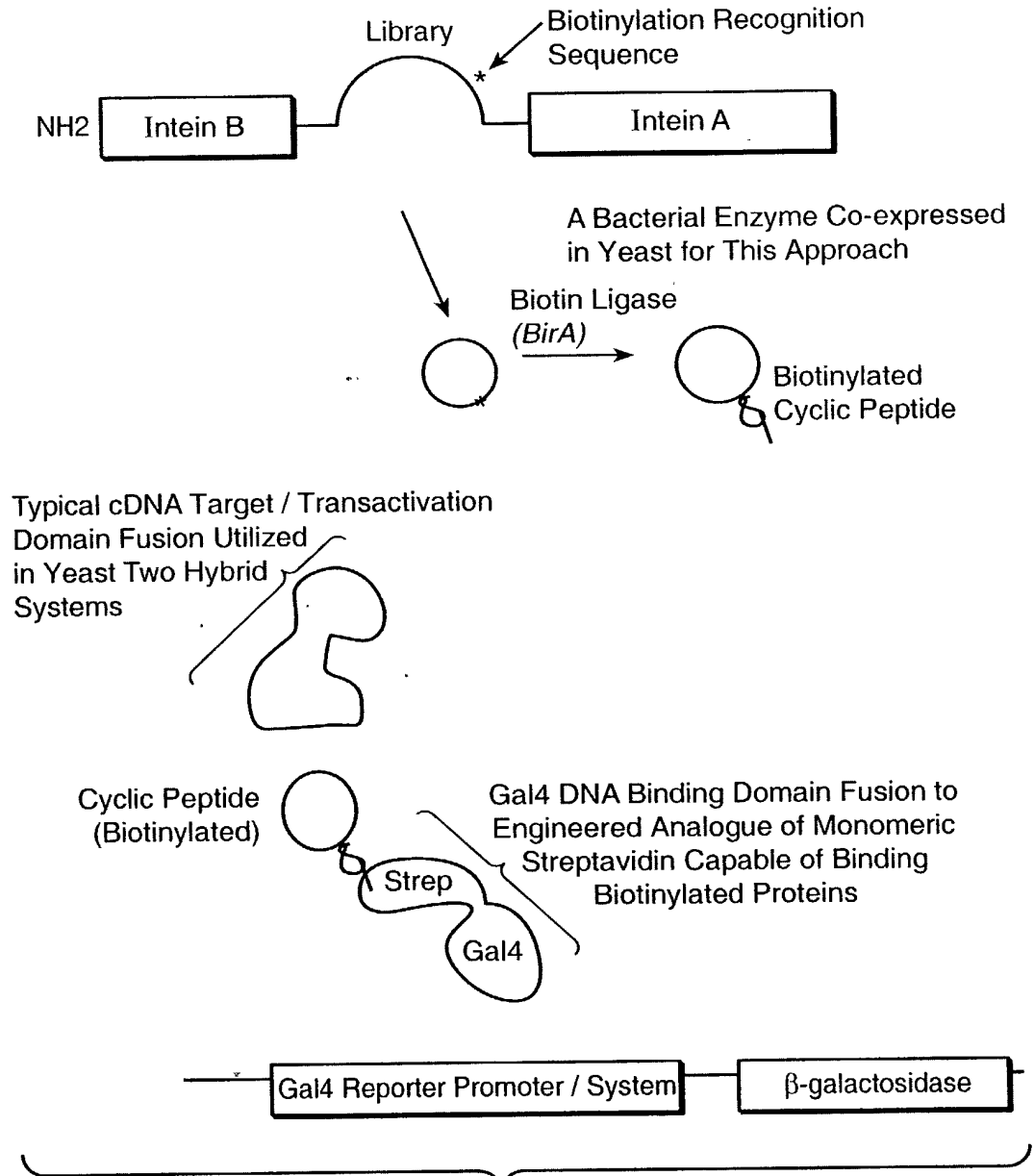
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**FIG.\_8**

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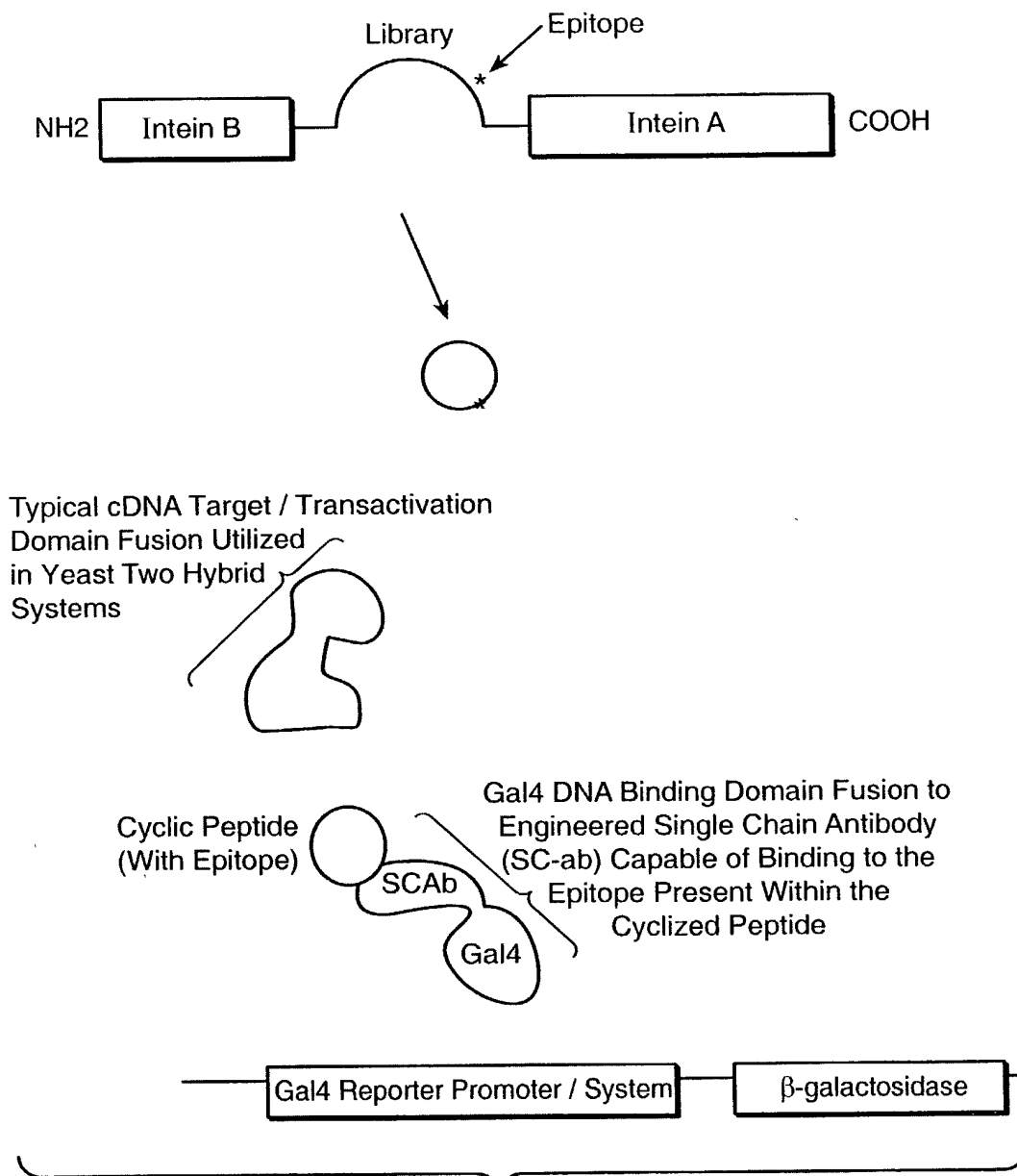
**FIG. 9**

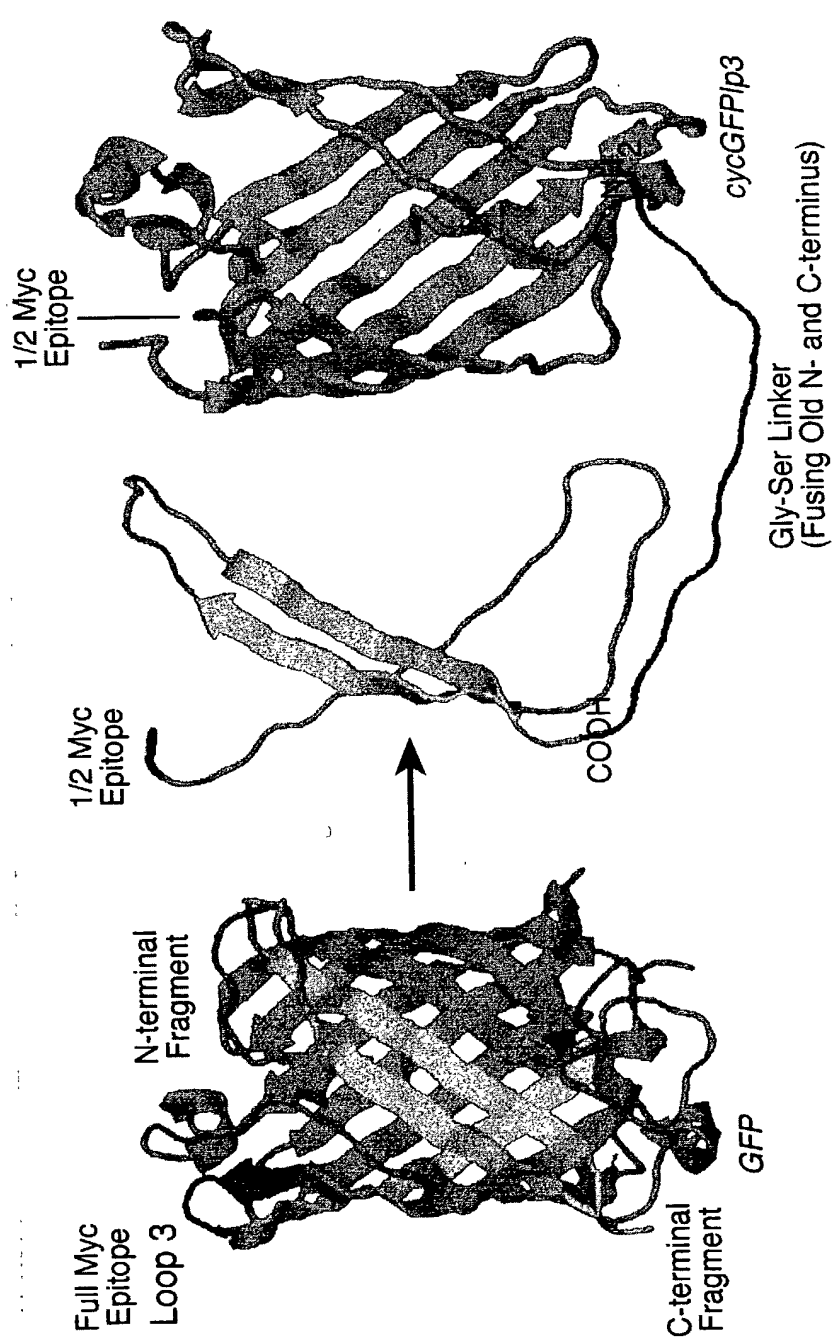
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**FIG. 10**

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**FIG. 11**



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IntB (Ic)  
 MESGSPEIEKLSQSDIYWDSIVSITETGVVEEVFDLTVPGP  
 myc<sup>6-10</sup>  
 HNFVANDIIVHNSEEDLGS SVQLADHYQQNTPIGDGPVLL  
 PDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDE  
 Gly-Ser Linker  
 LYKGSNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNG  
 GFP<sup>6-1-173</sup>  
 HKFSVSGEGEGDATYGLKTLKFICTTGKLPVPWPTLVTTL  
 TYGLQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDG  
 NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN  
 myc<sup>1-5</sup>  
 YNSHNVYIMADKQKNGIKVNFKIRHNIEDLEQKLICISGD  
 SLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLES AKV  
 IntA (In)  
 SRVFCTGKKLVYILKTRLGRTIKATANHRFLTIDGWKRLD  
 HA  
 ELSKLEHIALPRKLESSSLQLGLRGQYPYDVPDYAID

FIG. 12B

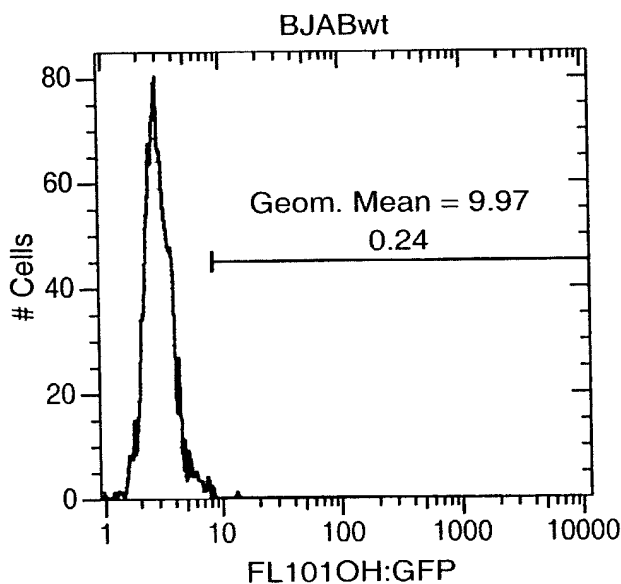


FIG. 12D-1

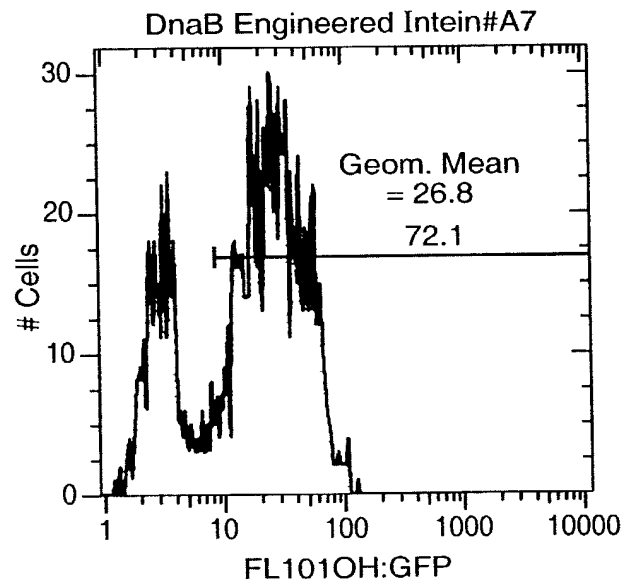


FIG. 12D-2

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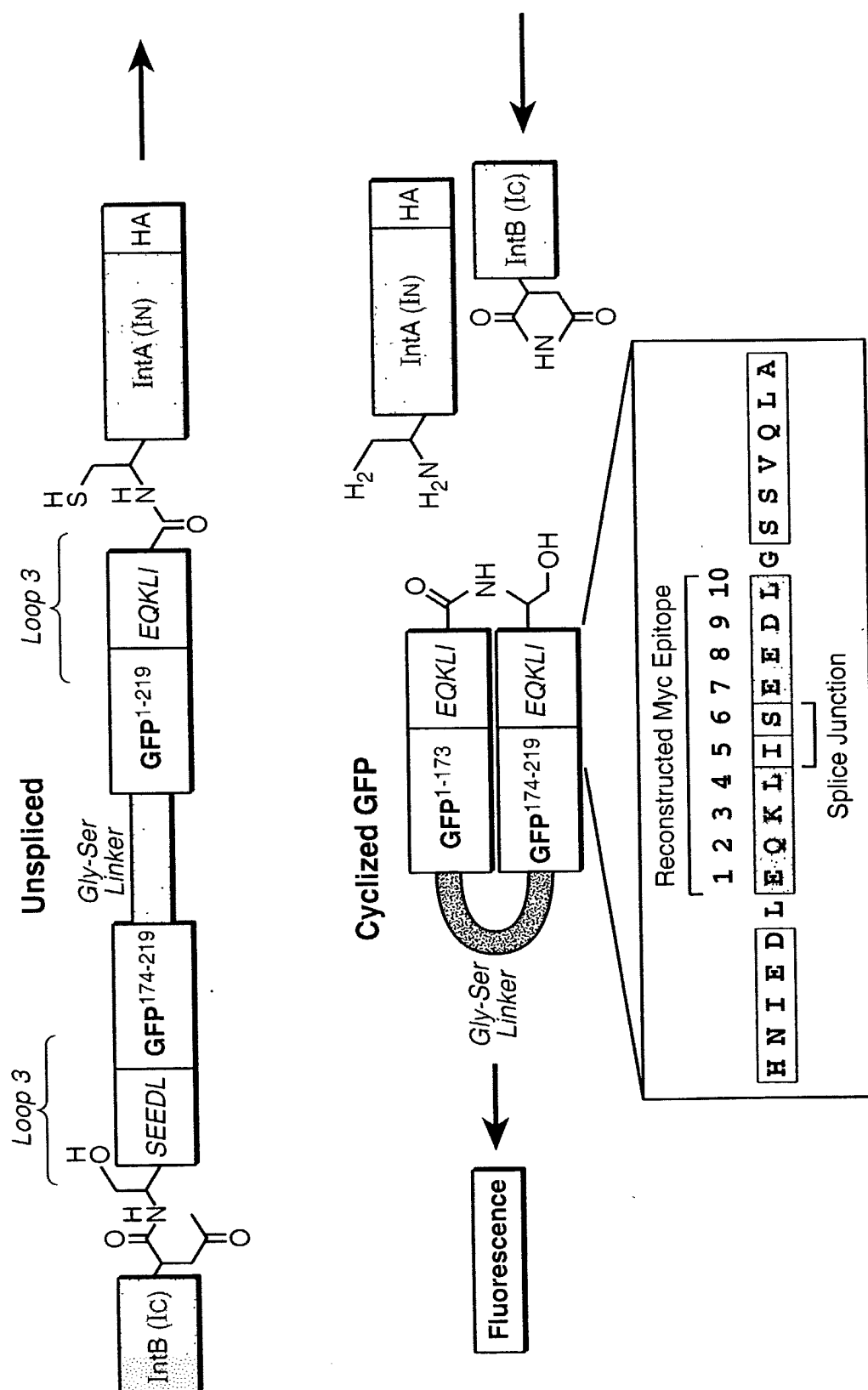


FIG. 12C-1



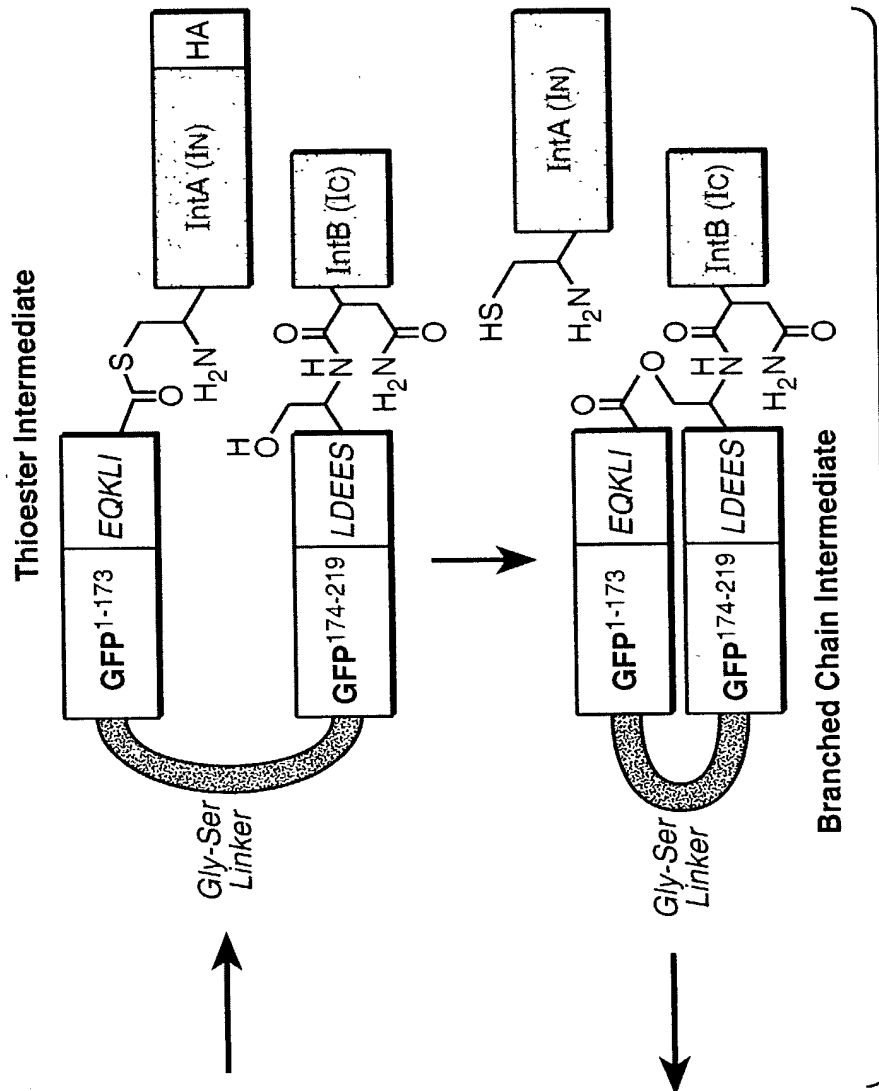
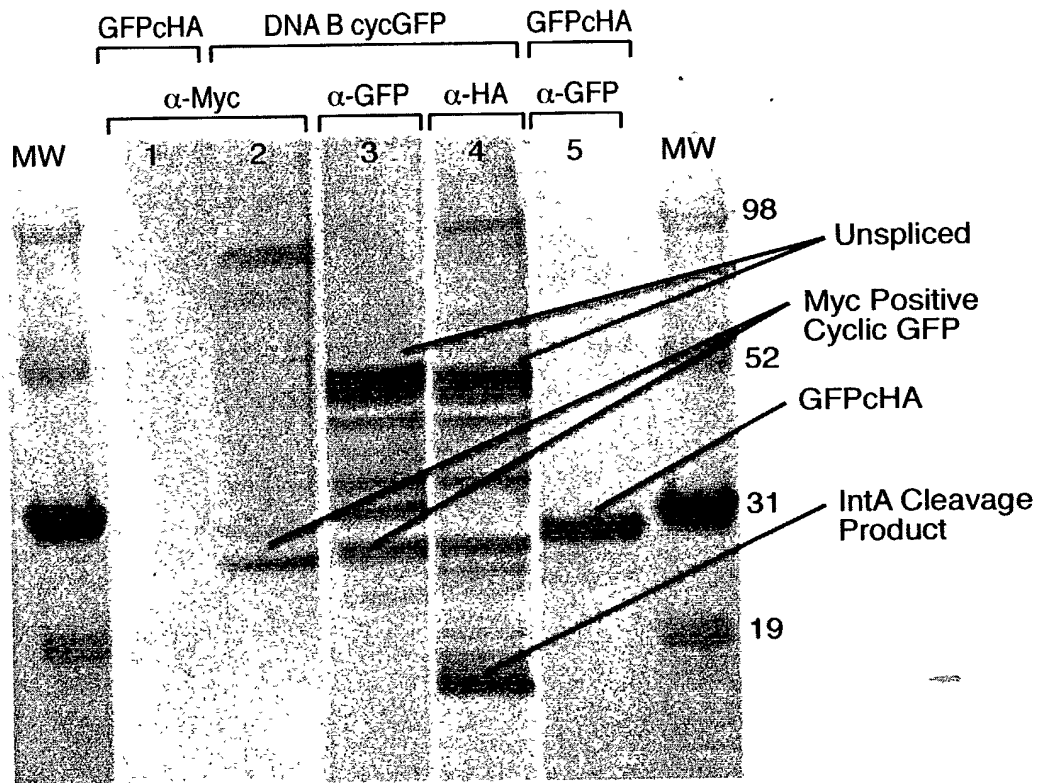
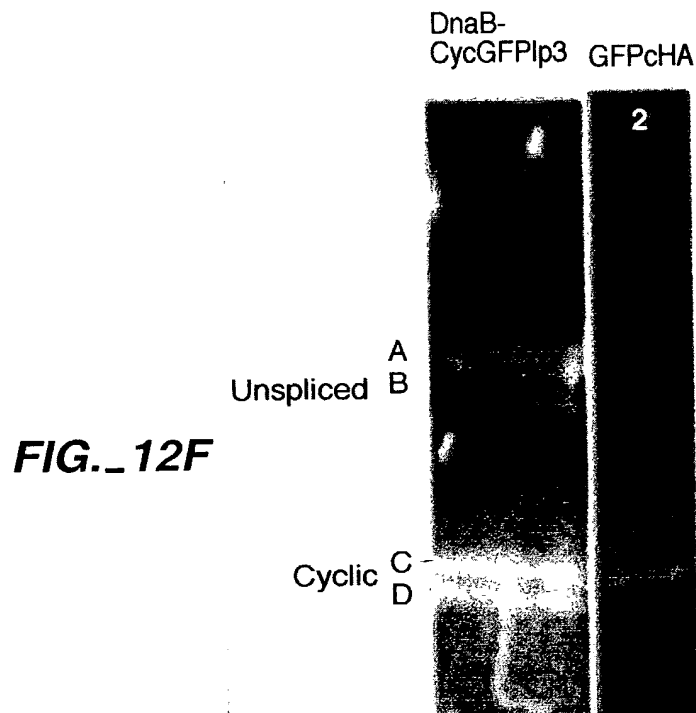


FIG..12C-2

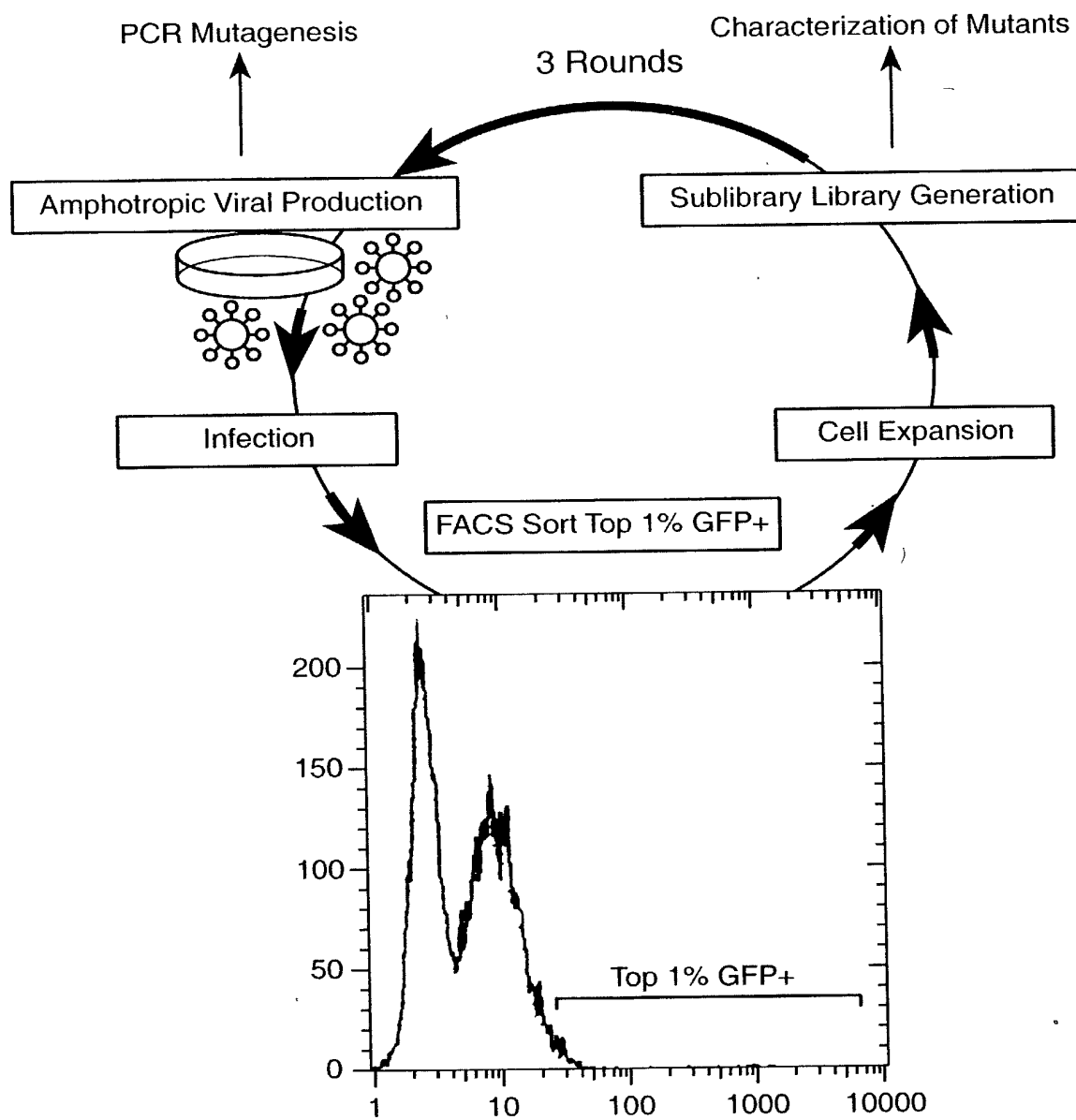


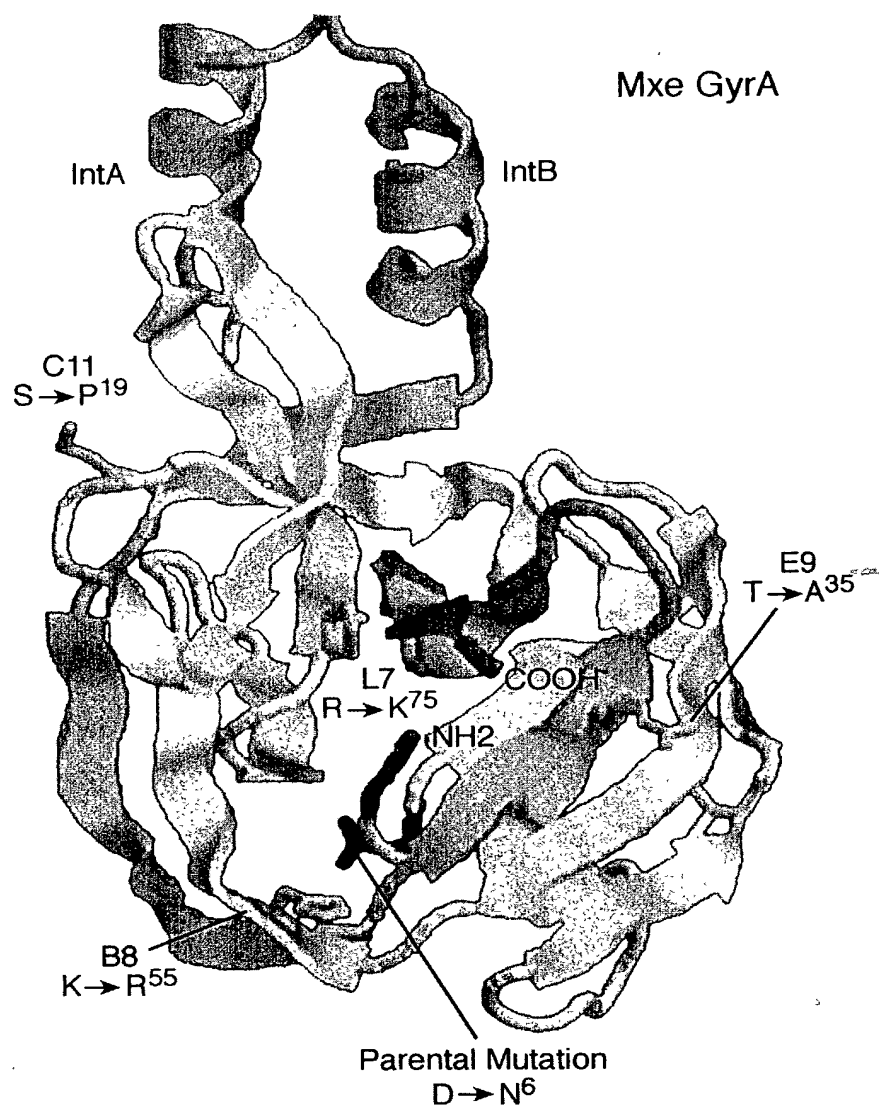
**FIG. 12E**



**FIG. 12F**

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**FIG. 13A**

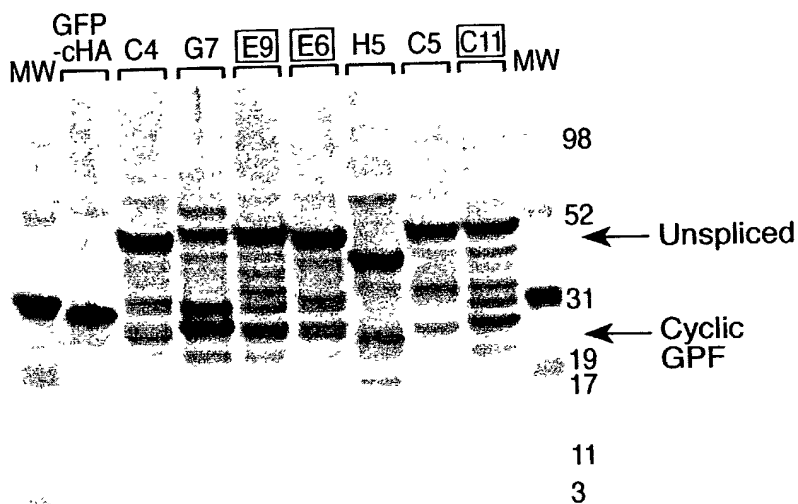


**FIG. 13B**

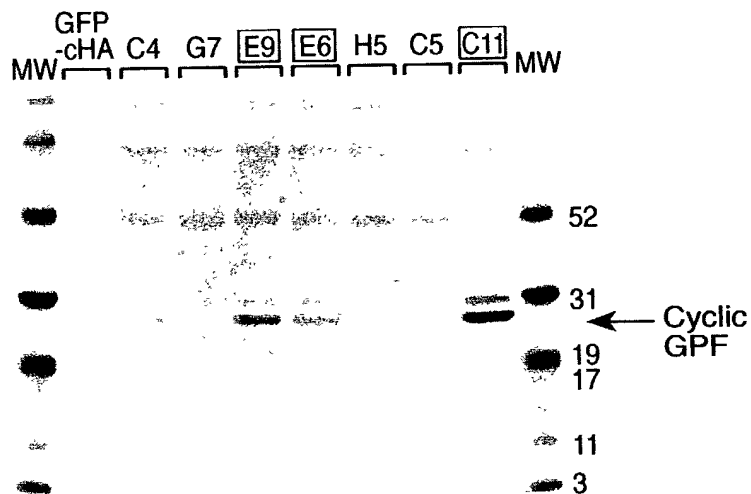


**FIG. 13C**

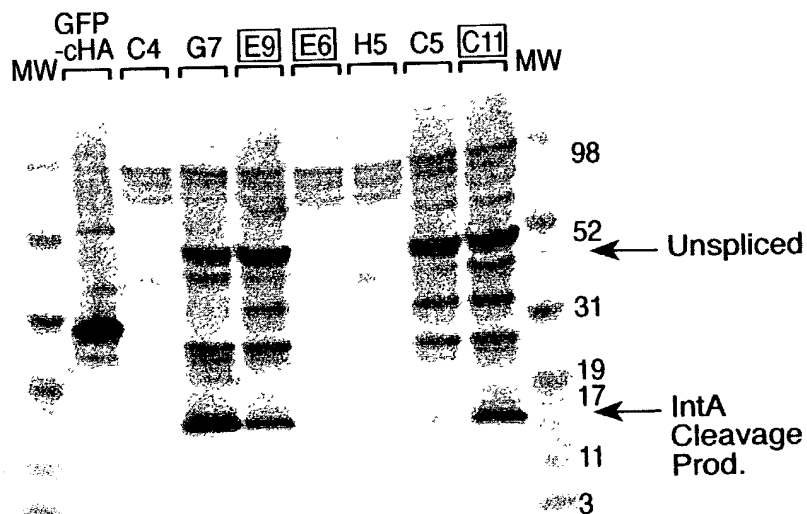
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**FIG.\_13D-1**

$\alpha$ -GFP  
Identifies All Splice Intermediates and Final Product

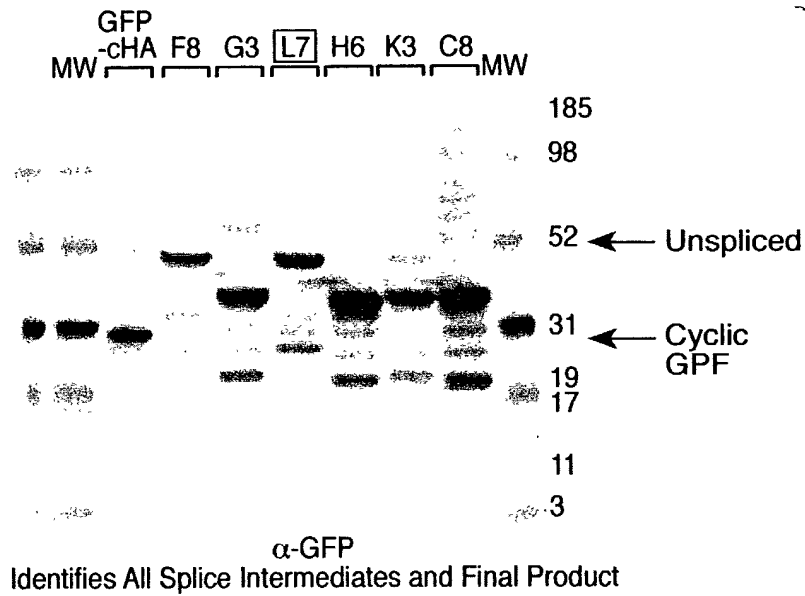
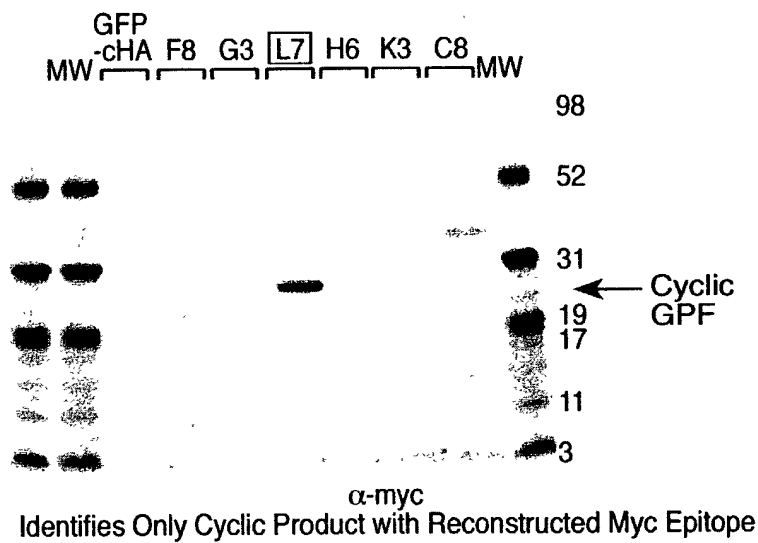
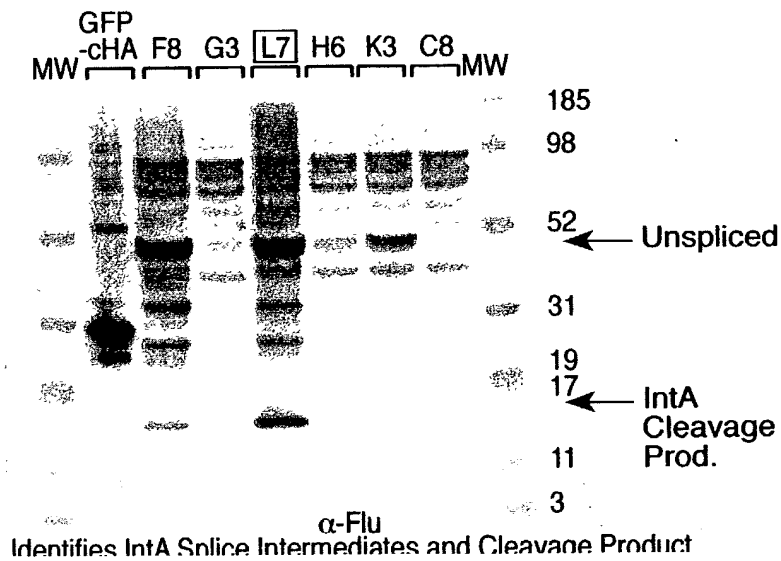
**FIG.\_13D-2**

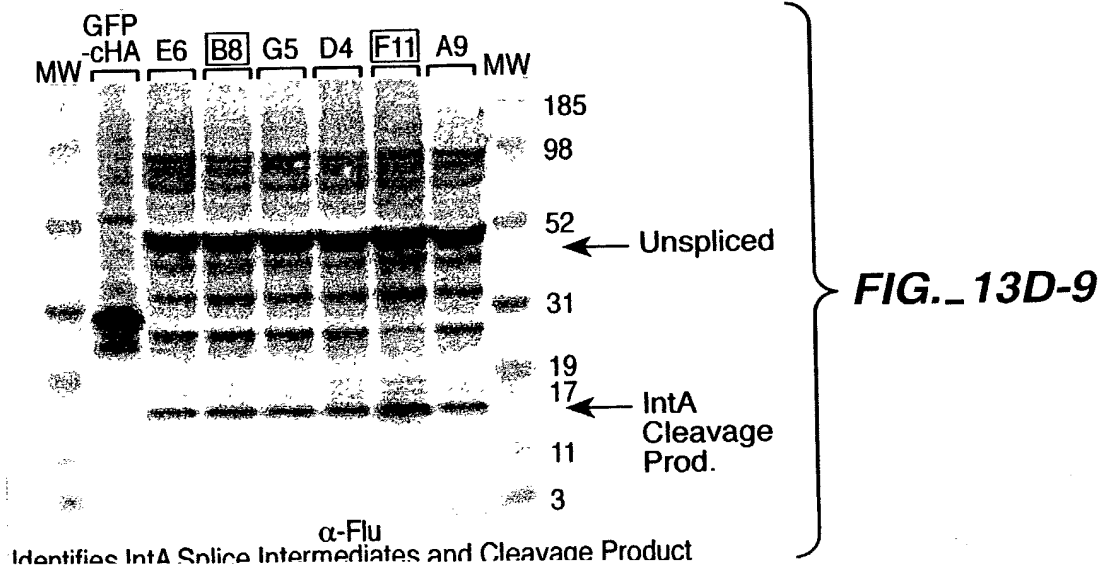
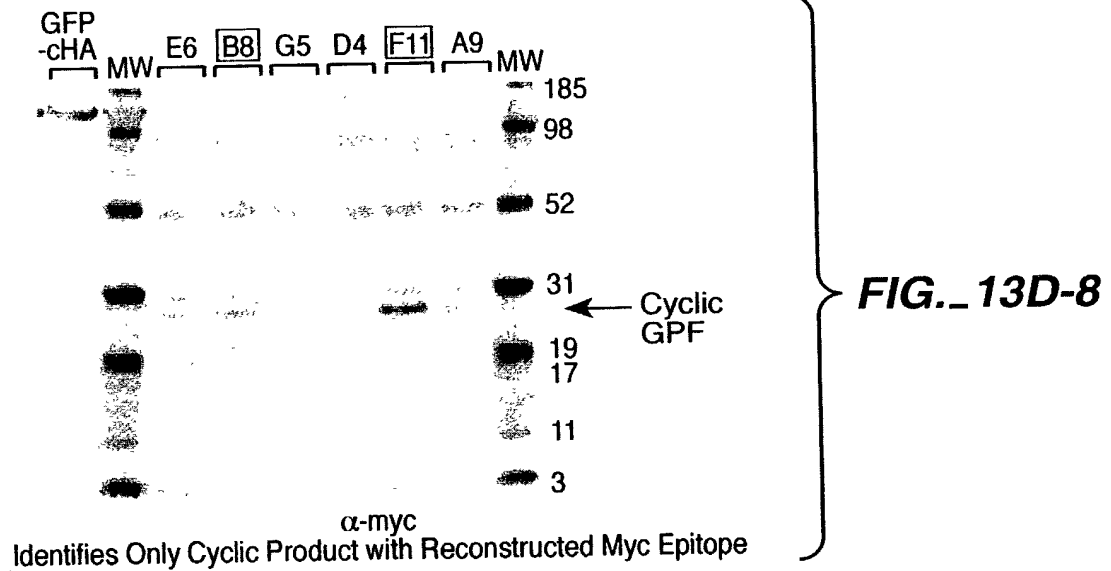
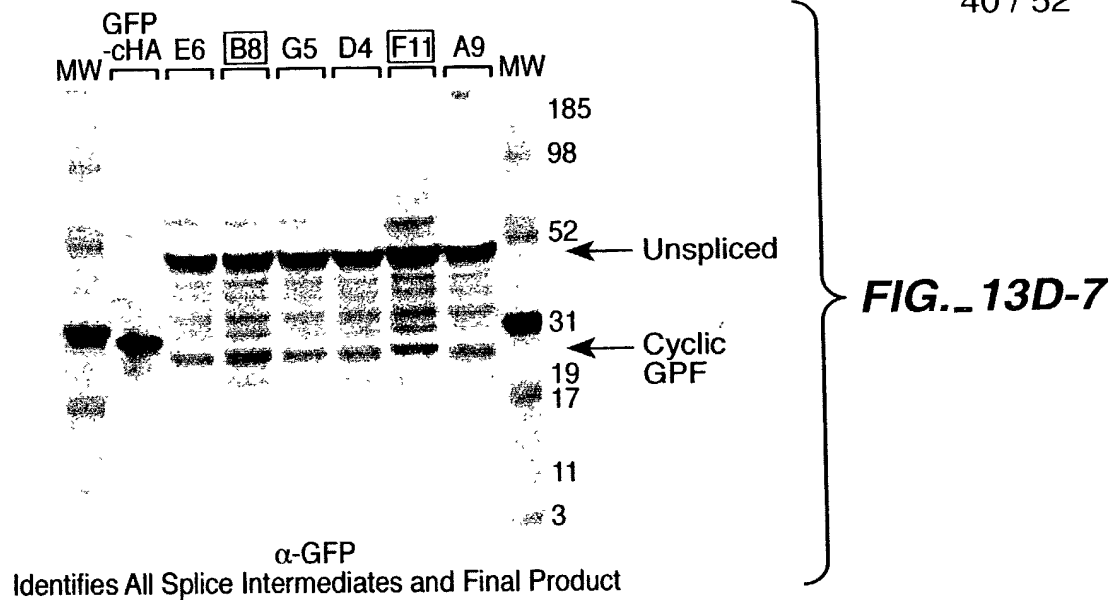
$\alpha$ -myc  
Identifies Only Cyclic Product with Reconstructed Myc Epitope

**FIG.\_13D-3**

$\alpha$ -Flu  
Identifies IntA Splice Intermediates and Cleavage Product

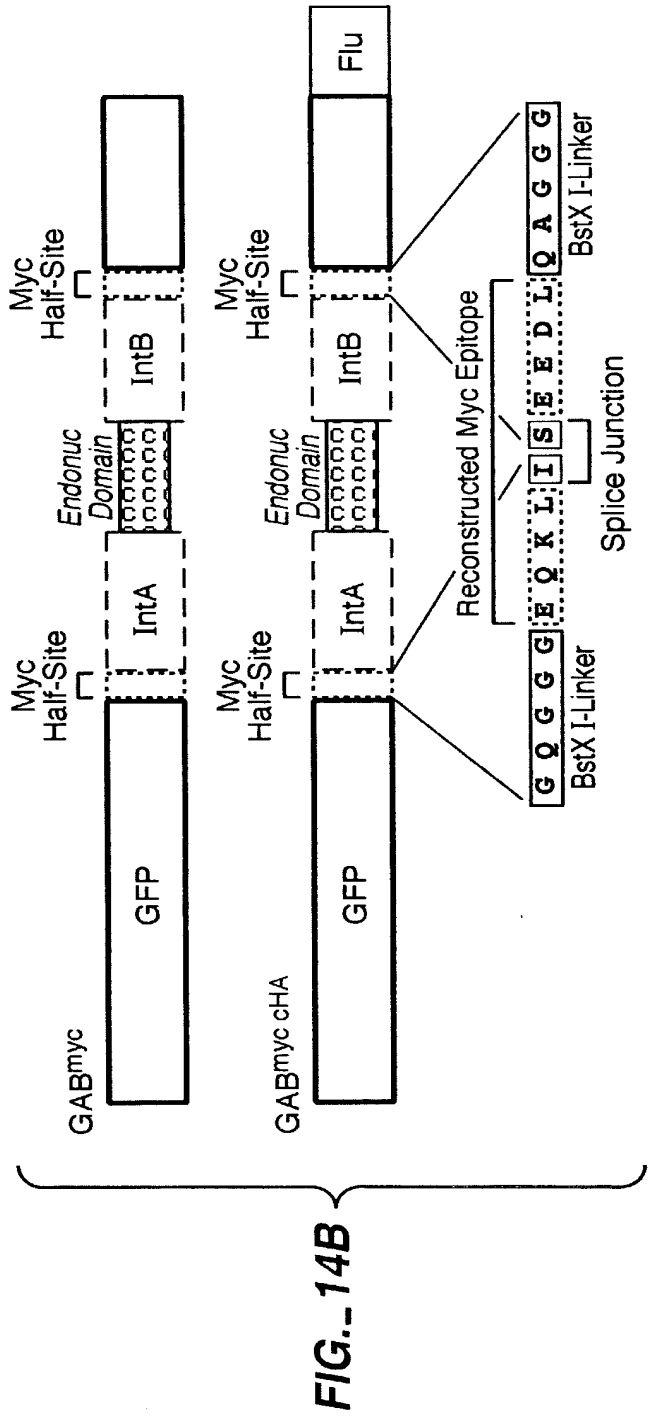
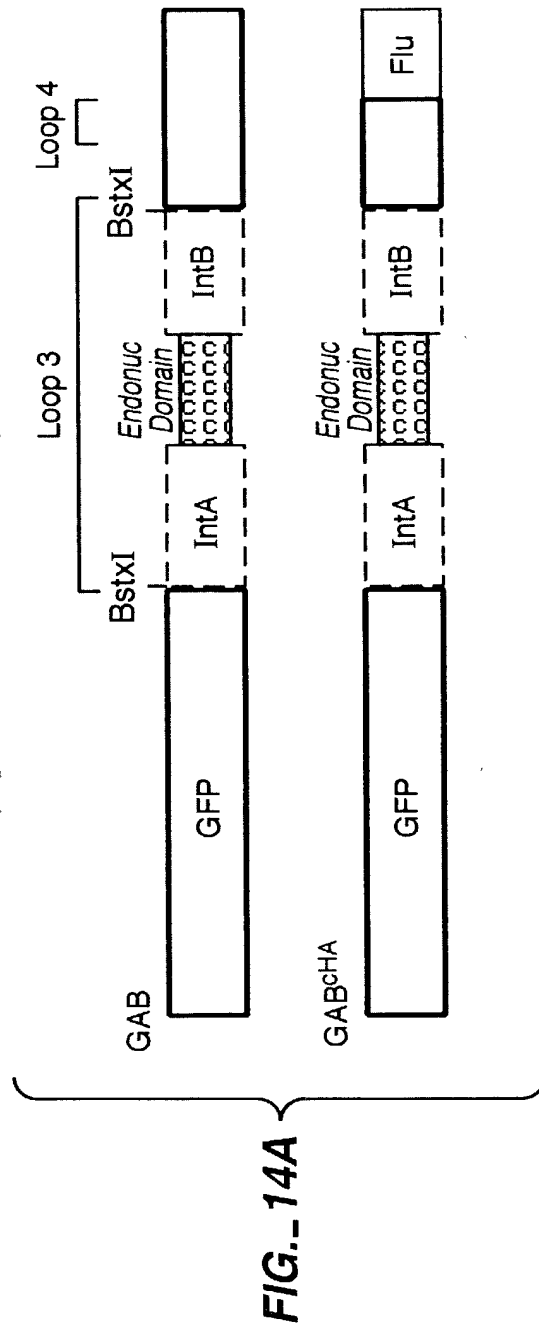
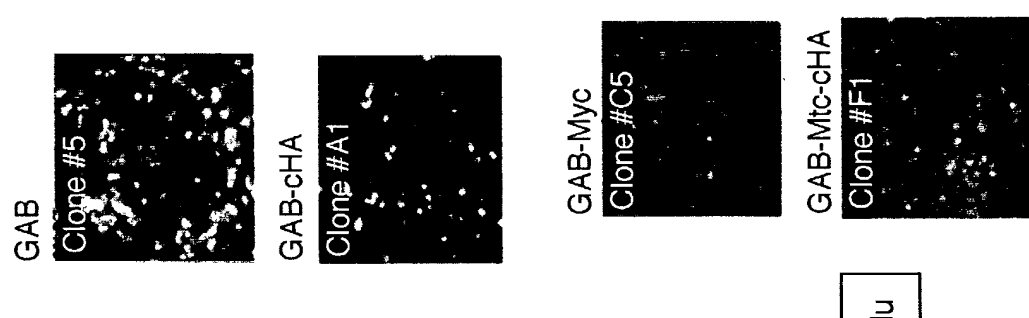
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**FIG.\_13D-4****FIG.\_13D-5****FIG.\_13D-6**

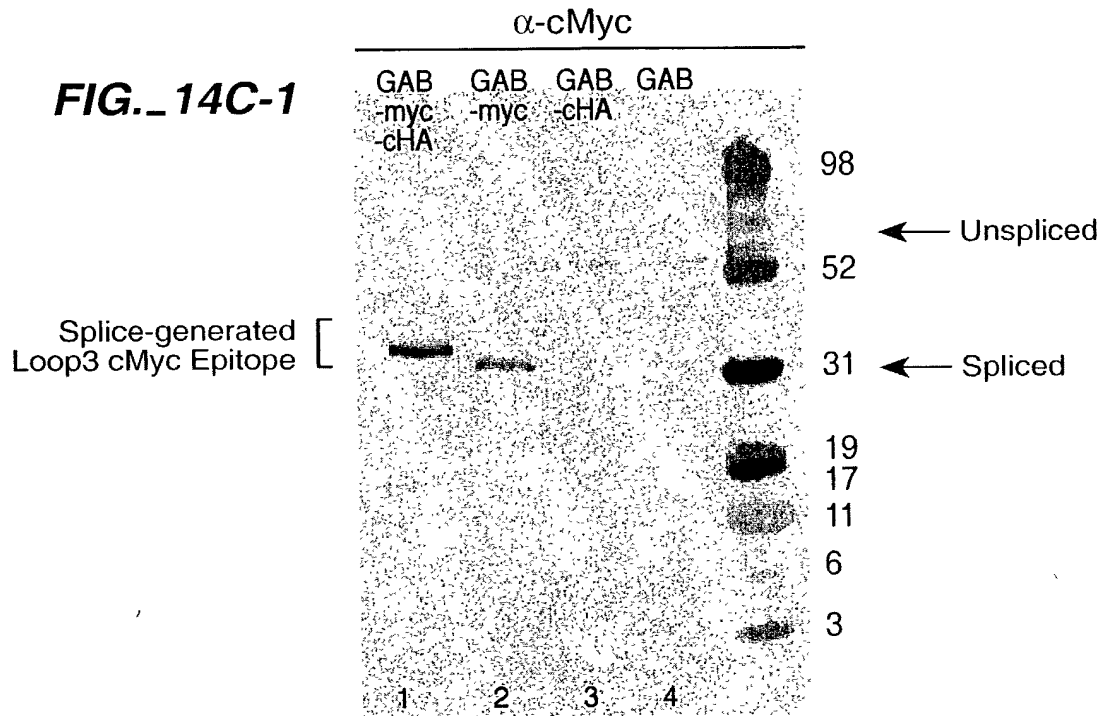
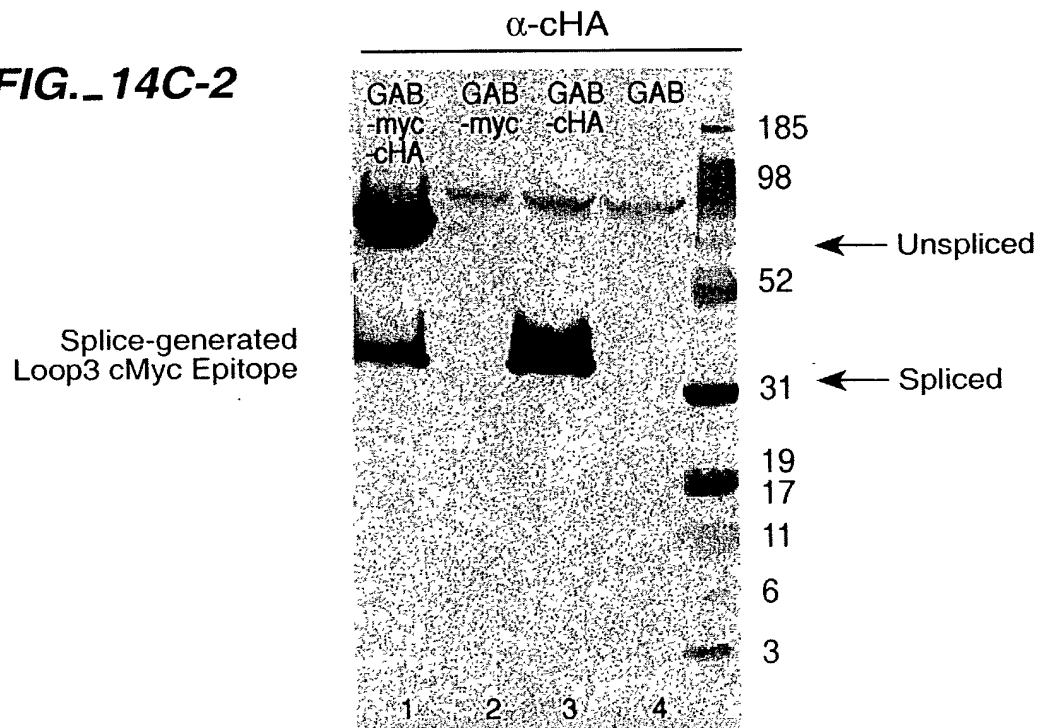




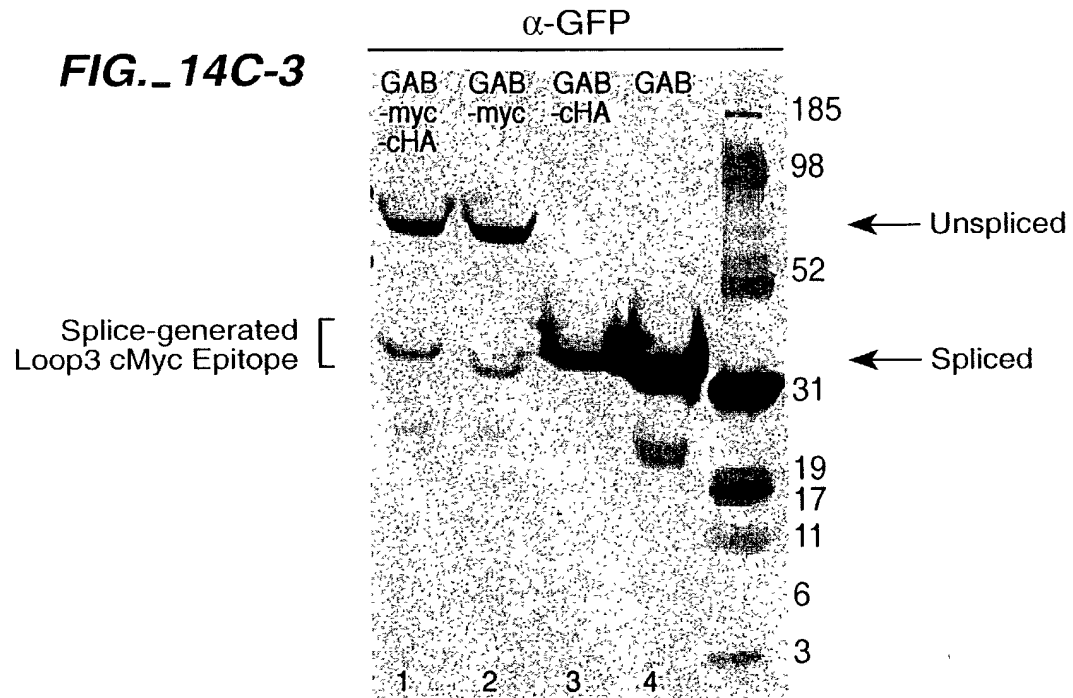
Transfected PhxX Cells



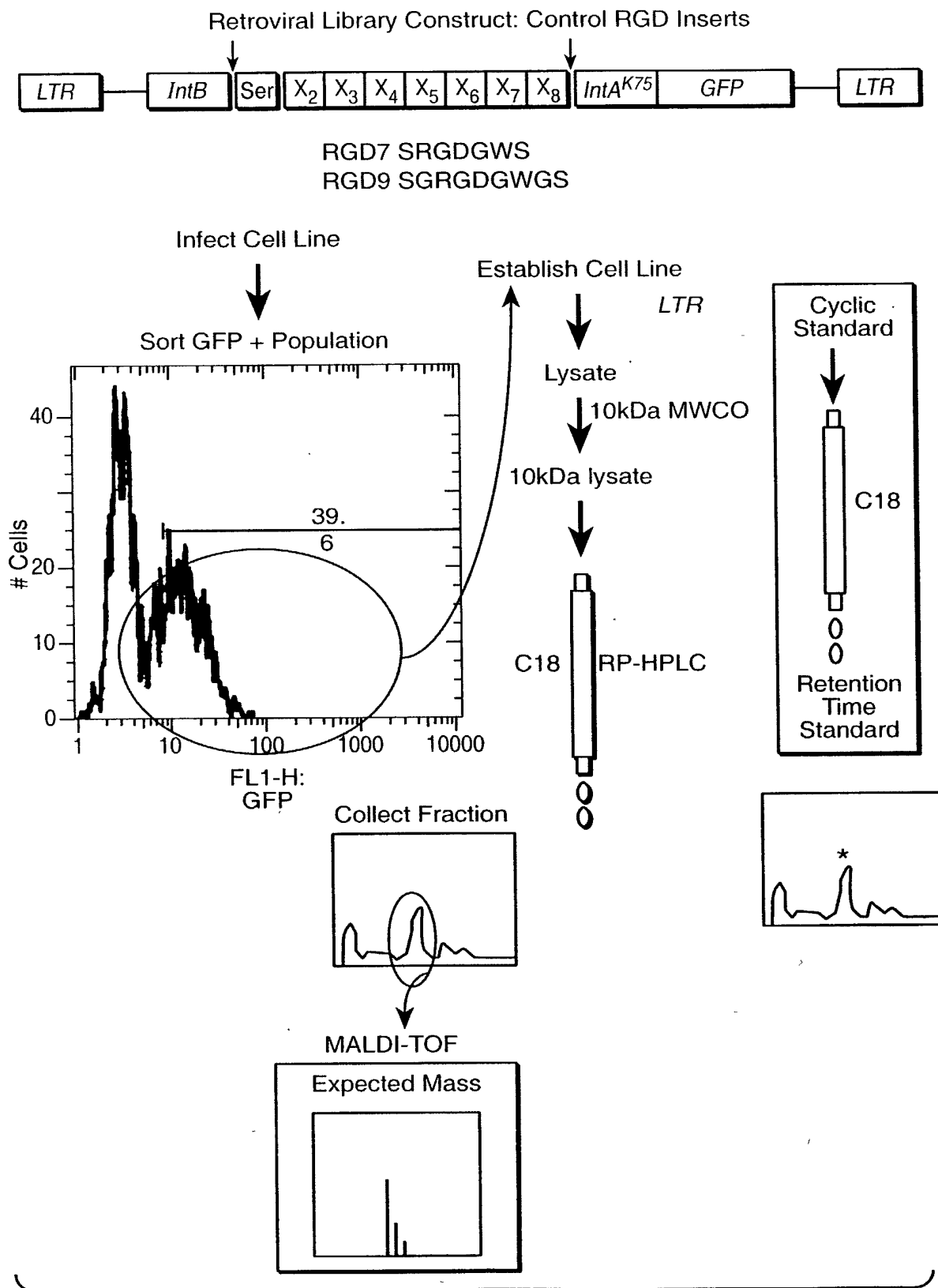
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**FIG.\_14C-1****FIG.\_14C-2**

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**FIG.\_14C-3**

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**FIG. 15A**

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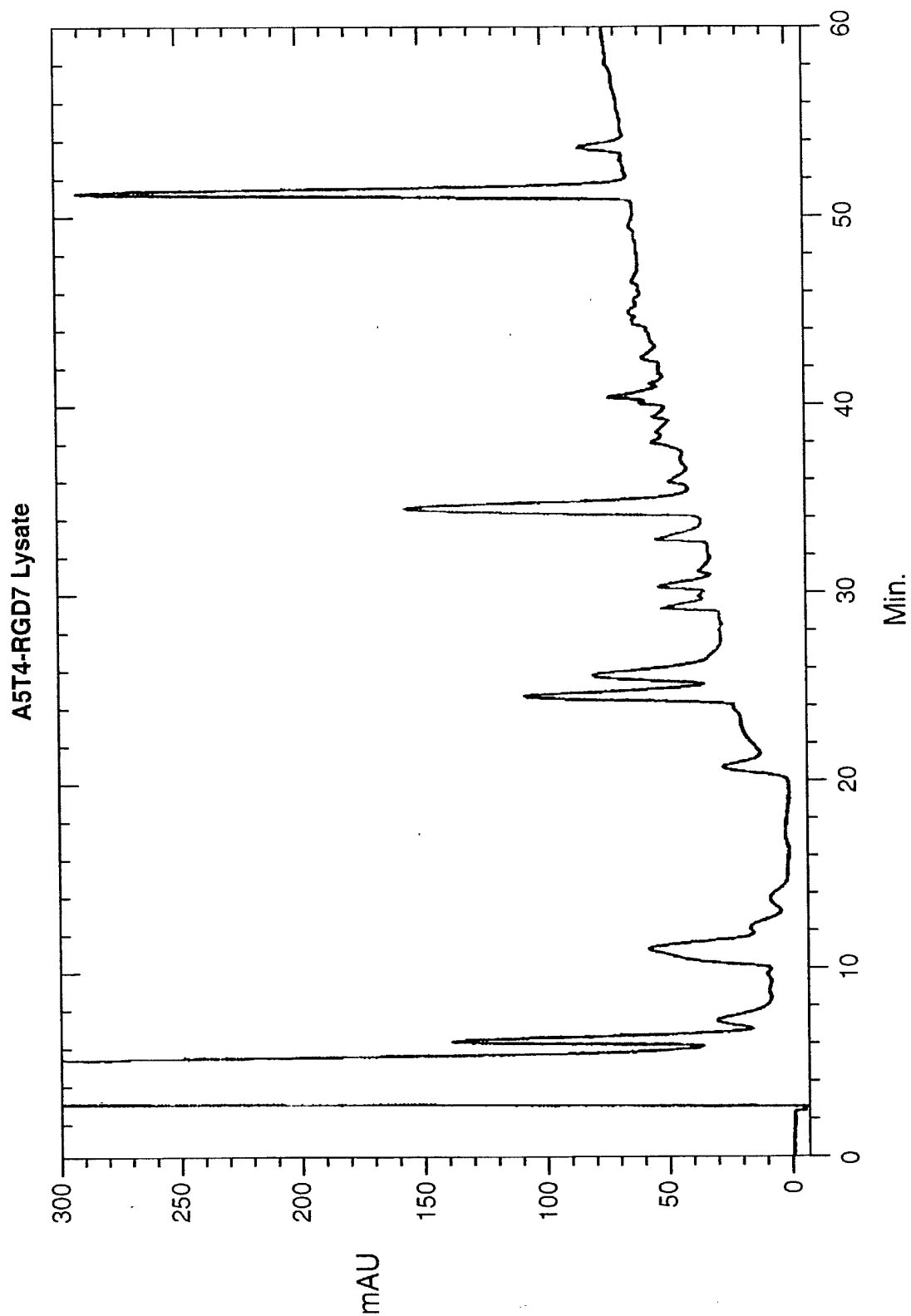
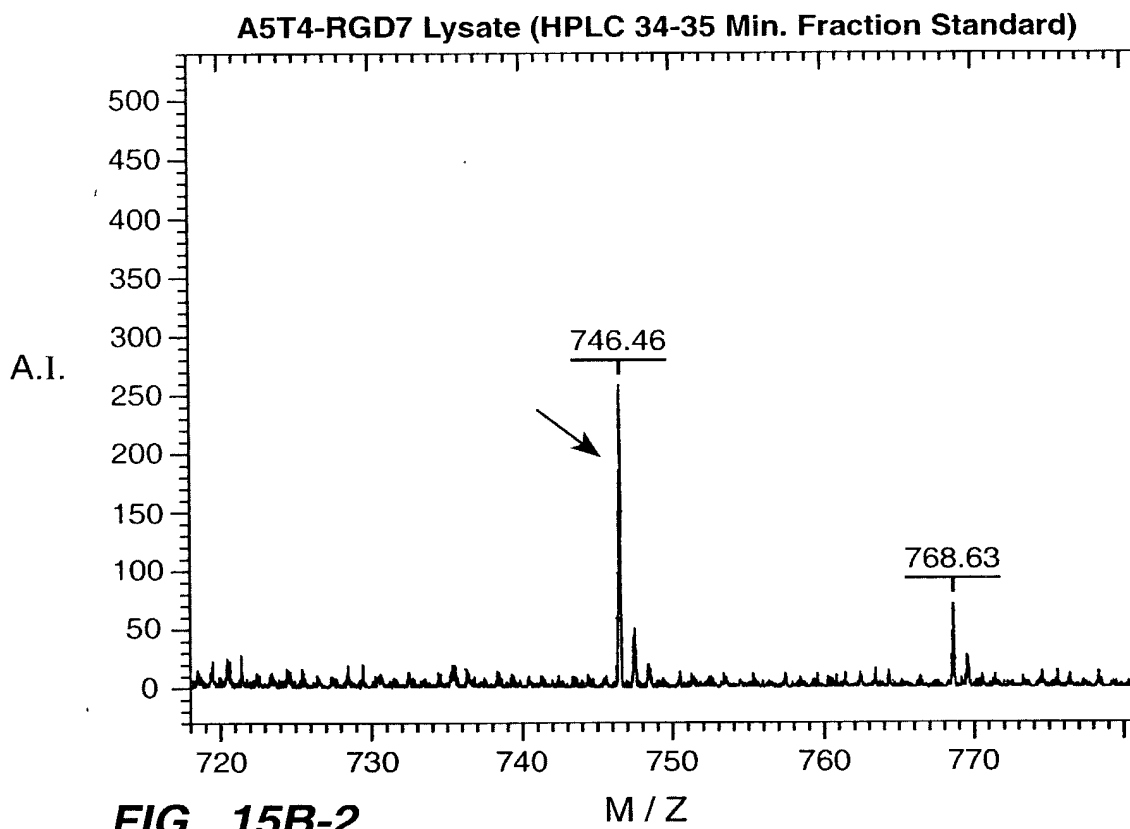
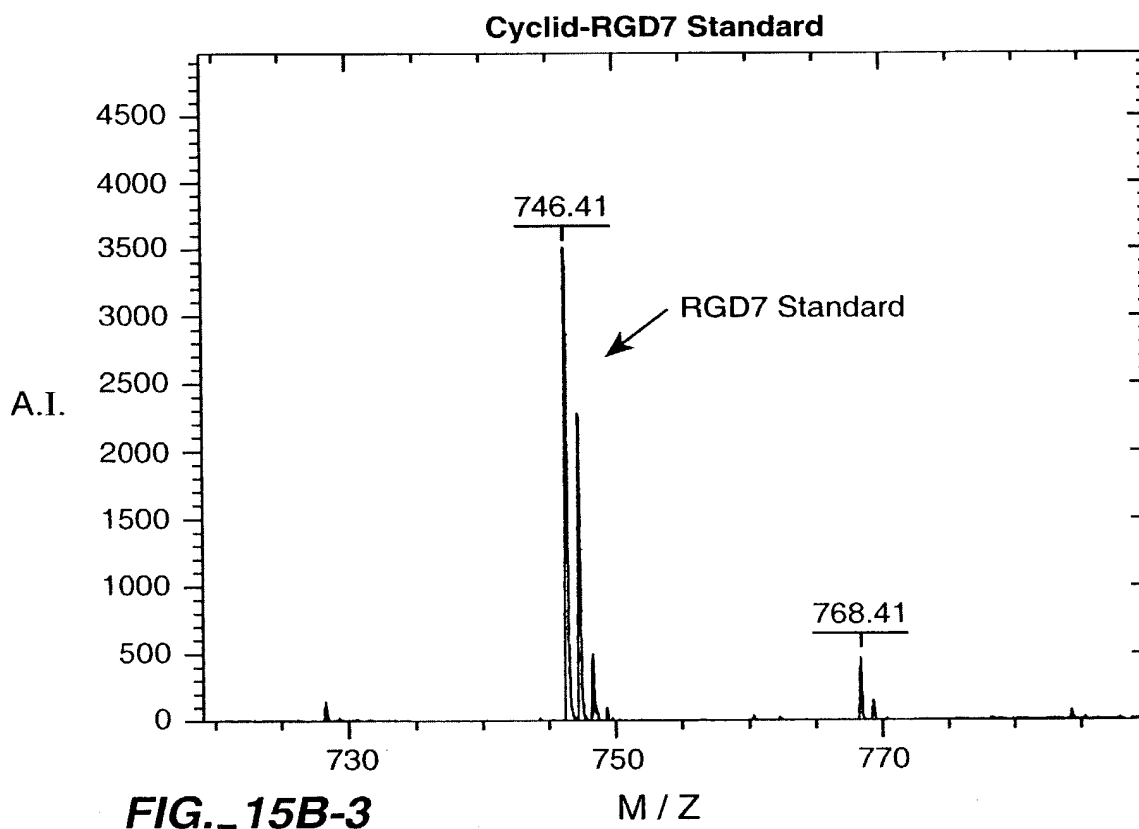


FIG.. 15B-1

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**FIG.\_15B-2****FIG.\_15B-3**

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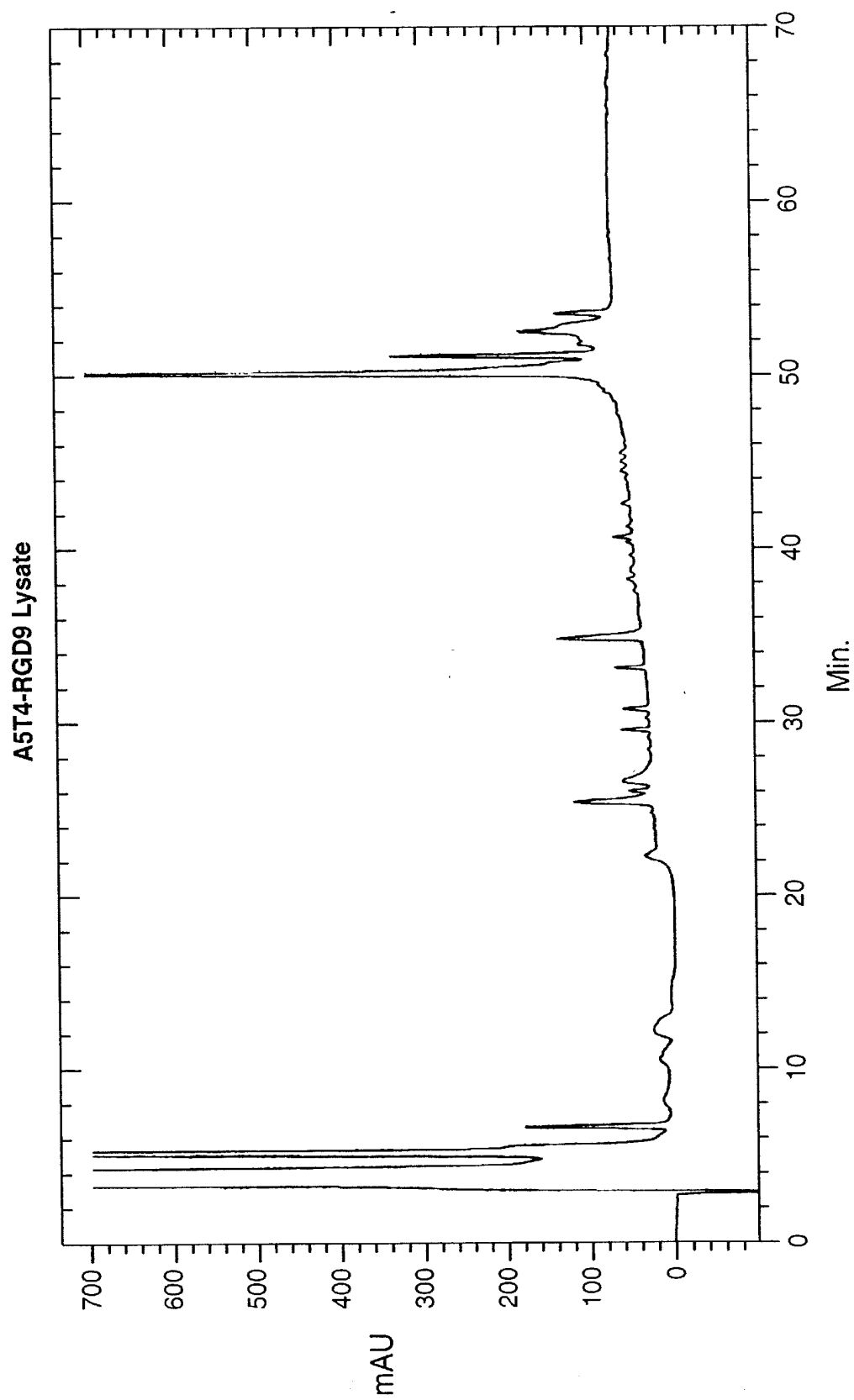
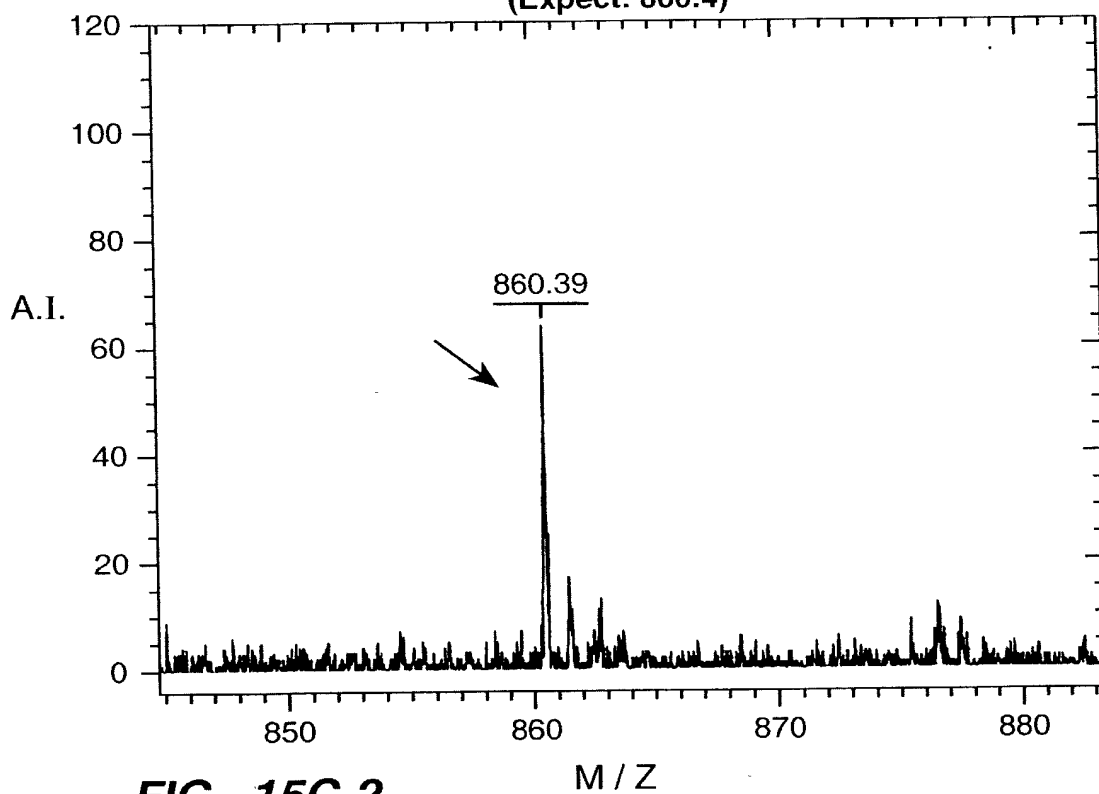
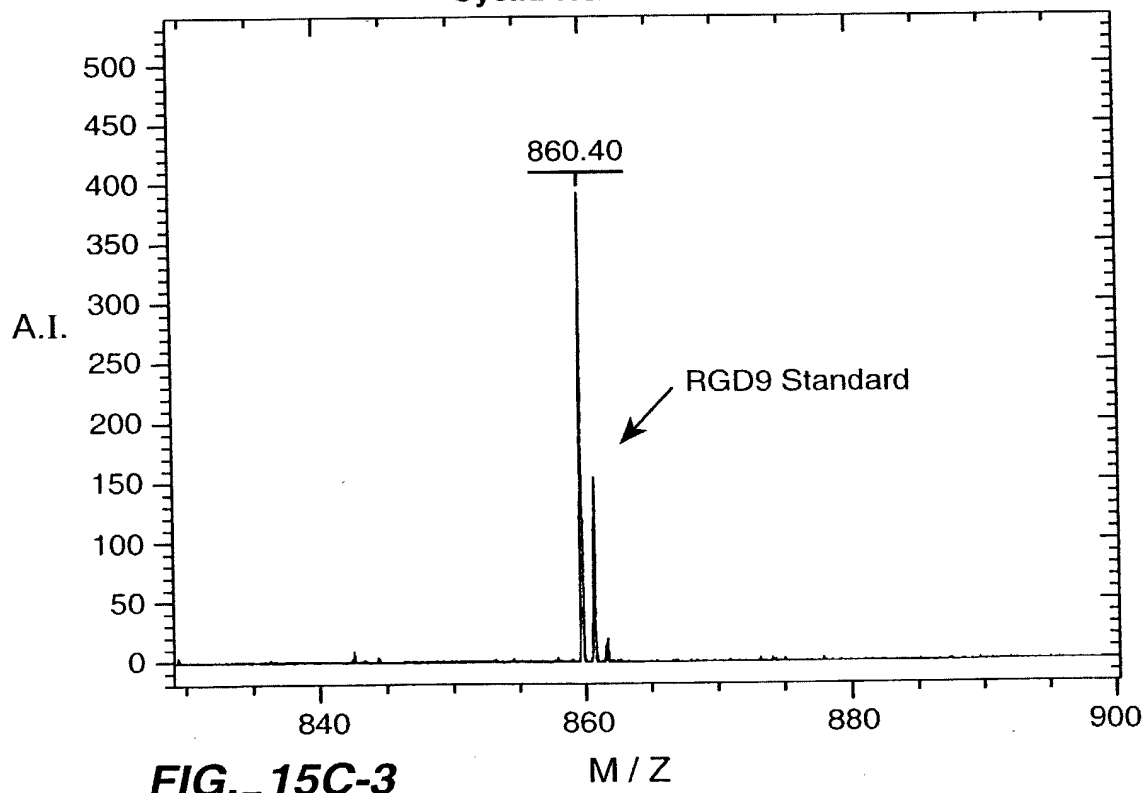


FIG.\_15C-1

A5T4-RGD7 Lysate (HPLC 33-34 Min. Fraction Standard)  
(Expect: 860.4)

**FIG.\_15C-2**

Cyclid-RGD9 Standard

**FIG.\_15C-3**



